FIGURE 1A

```
   1 TGGAAGGGTT AATTTACTCC AAGAAAAGGC AAGAAATCCT TGATTTGTGG GTCTATCACA
  61 CACAAGGCTT CTTCCCTGAT TGGCAAAACT ACACACCGGG GCCAGGGGTC AGATATCCAC
 121 TGACCTTTGG ATGGTGCTAC AAGCTAGTGC CAGTTGACCC AGGGGAGGTG GAAGAGGCCA
 181 ACGGAGGAGA AGACAACTGT TTGCTACACC CTATGAGCCA ACATGGAGCA GAGGATGAAG
 241 ATAGAGAAGT ATTAAAGTGG AAGTTTGACA GCCTCCTAGC ACGCAGACAC ATGGCCCGCG
 301 AGCTACATCC GGAGTATTAC AAAGACTGCT GACACAGAAG GGACTTTCCG CCTGGGACTT
 361 TCCACTGGGG CGTTCCGGGA GGTGTGGTCT GGGCGGGACT GGGAGTGGT CAACCCTCAG
 421 ATGCTGCATA TAAGCAGCTG CTTTTCGCCT GTACTGGGTC TCTCTGGTA GACCAGATCT
 481 GAGCCTGGGA GCCCTCTGGC TATCTAGGGA ACCCACTGCT TAAGCCTCAA TAAAGCTTGC
 541 CTTGAGTGCT TTAAGTAGTG TGTGCCCATC TGTTGTGTGA CTCTGGTAAC TAGAGATCCC
 601 TCAGACCCTT TGTGGTAGTG TGGAAAATCT CTAGCAGTGG CGCCCGAACA GGGACCAGAA
 661 AGTGAAAGTG AGACCAGAGG AGATCTCTCG ACGCAGGACT CGGCTTGCTG AAGTGCACAC
 721 GGCAAGAGGC GAGAGGGGCG GCTGGTGAGT ACGCCAATTT TACTTGACTA GCGGAGGCTA
 781 GAAGGAGAGA GATGGGTGCG AGAGCGTCAA TATTAAGCGG CGGAAAATTA GATAAATGGG
 841 AAAGAATTAG GTTAAGGCCA GGGGGAAAGA AACATTATAT GTTAAAACAT CTAGTATGGG
 901 CAAGCAGGGA GCTGGAAAGA TTTGCACTTA ACCCTGGCCT GTTAGAAACA TCAGAAGGCT
 961 GTAAACAAAT AATAAAACAG CTACAACCAG CTCTTCAGAC AGGAACAGAG GAACTTAGAT
1021 CATTATTCAA CACAGTAGCA ACTCTCTATT GTGTACATAA AGGGATAGAG GTACGAGACA
1081 CCAAGGAAGC CTTAGACAAG ATAGAGGAAG AACAAAACAA ATGTCAGCAA AAAGCACAAC
1141 AGGCAAAAGC AGCTGACGAA AAGGTCAGTC AAAATTATCC TATAGTACAG AATGCCCAAG
1201 GGCAAATGGT ACACCAAGCT ATATCACCTA GAACATTGAA TGCATGGATA AAAGTAATAG
1261 AGGAAAAGGC TTTCAATCCA GAGGAAATAC CCATGTTTAC AGCATTATCA GAAGGAGCCA
1321 CCCCACAAGA TTTAAACACA ATGTTAAATA CAGTGGGGGG ACATCAAGCA GCCATGCAAA
1381 TGTTAAAAGA TACCATCAAT GAGGAGGCTG CAGAATGGGA TAGGACACAT CCAGTACATG
1441 CAGGGCCTGT TGCACCAGGC CAGATGAGAG AACCAAGGGG AAGTGACATA GCAGGAACTA
1501 CTAGTACCCT TCAGGAACAA ATAGCATGGA TGACAAGTAA TCCACCTATT CCAGTAGAAG
1561 ACATCTATAA AAGATGGATA ATTCTGGGGT TAAATAAAAT AGTAAGAATG TATAGCCCTG
1621 TTAGCATTTT GGACATAAAA CAAGGGCCAA AGAACCCTT TAGAGACTAT GTAGACCGGT
1681 TCTTTAAAAC CTTAAGAGCT GAACAAGCTA CACAAGATGT AAAGAATTGG ATGACAGACA
1741 CCTTGTTGGT CCAAAATGCG AACCCAGATT GTAAGACCAT TTTAAGAGCA TTAGGACCAG
1801 GGGCCTCATT AGAAGAAATG ATGACAGCAT GTCAGGGAGT GGGAGGACCT AGCCATAAAG
1861 CAAGAGTGTT GGCTGAGGCA ATGAGCCAAG CAAACAGTAA CATACTAGTG CAGAGAAGCA
1921 ATTTTAAAGG CTCTAACAGA ATTATTAAAT GTTTCAACTG TGGCAAAGTA GGGCACATAG
1981 CCAGAAATTG CAGGGCCCCT AGGAAAAAGG CTGTTGGAA ATGTGGACAG GAAGGACACC
2041 AAATGAAAGA CTGTACTGAG AGGCAGGCTA ATTTTTTAGG GAAAATTTGG CCTTCCCACA
2101 AGGGGAGGCC AGGGAATTTC CTCCAGAACA GACCAGAGCC AACAGCCCCA CCAGCAGAAC
2161 CAACAGCCCC ACCAGCAGAG AGCTTCAGGT TCGAGGAGAC AACCCCCGTG CCGAGGAAGG
2221 AGAAAGAGAG GAACCTTTA ACTTCCCTCA AATCACTCTT TGGCAGCGAC CCCTTGTCTC
2281 AATAAAAGTA GAGGGCCAGA TAAAGGAGGC TCTCTTAGAC ACAGGAGCAG ATGATACAGT
2341 ATTAGAAGAA ATAGATTTGC CAGGGAAATG GAAACCAAAA ATGATAGGGG GAATTGGAGG
2401 TTTTATCAAA GTAAGACAGT ATGATCAAAT ACTTATAGAA ATTTGTGGAA AAAAGGCTAT
2461 AGGTACAGTA TTAGTAGGGC CTACACCAGT CAACATAATT GGAAGAAATC TGTTAACTCA
2521 GCTTGGATGC ACACTAAATT TTCCAATTAG TCCTATTGAA ACTGTACCAG TAAAATTAAA
2581 ACCAGGAATG GATGGCCCAA AGGTCAAACA ATGGCCATTG ACAGAAGAAA AAATAAAAGC
2641 ATTAACAGCA ATTTGTGAGG AAATGGAGAA GGAAGGAAAA ATTACAAAAA TTGGGCCTGA
2701 TAATCCATAT AACACTCCAG TATTTGCCAT AAAAAAGAAG GACAGTACTA AGTGGAGAAA
2761 ATTAGTAGAT TTCAGGGAAC TCAATAAAAG AACTCAAGAC TTTTGGGAAG TTCAATTAGG
2821 AATACCACAC CCAGCAGGAT TAAAAAAGAA AAATCAGTG ACAGTGCTAG ATGTGGGGGA
2881 TGCATATTTT TCAGTTCCTT TAGATGAAAG CTTCAGGAAA TATACTGCAT TCACCATACC
2941 TAGTATAAAC AATGAAACAC CAGGGATTAG ATATCAATAT AATGTGCTGC CACAGGGATG
3001 GAAAGGATCA CCAGCAATAT TCCAGAGTAG CATGACAAAA ATCTTAGAGC CCTTCAGAGC
3061 AAAAAATCCA GACATAGTTA TCTATCAATA TATGGATGAC TTGTATGTAG GATCTGACTT
3121 AGAAATAGGG CAACATAGAG CAAAAATAGA GAGTTAAGG GAACATTTAT TGAAATGGGG
```

FIGURE 1B

```
3181 ATTTACAACA CCAGACAAGA AACATCAAAA AGAACCCCCA TTTCTTTGGA TGGGGTATGA
3241 ACTCCATCCT GACAAATGGA CAGTACAACC TATACTGCTG CCAGAAAAGG ATAGTTGGAC
3301 TGTCAATGAT ATACAGAAGT TAGTGGGAAA ATTAAACTGG GCAAGTCAGA TTTACCCAGG
3361 GATTAAAGTA AGGCAACTCT GTAAACTCCT CAGGGGGGCC AAAGCACTAA CAGACATAGT
3421 ACCACTAACT GAAGAAGCAG AATTAGAATT GGCAGAGAAC AGGGAAATTT TAAGAGAACC
3481 AGTACATGGA GTATATTATG ATCCATCAAA AGACTTGATA GCTGAAATAC AGAAACAGGG
3541 GCATGAACAA TGGACATATC AAATTTATCA AGAACCATTT AAAAATCTGA AAACAGGGAA
3601 GTATGCAAAA ATGAGGACTA CCCACACTAA TGATGTAAAA CAGTTAACAG AGGCAGTGCA
3661 AAAAATAGCC ATGGAAAGCA TAGTAATATG GGGAAAGACT CCTAAATTTA GACTACCCAT
3721 CCAAAAAGAA ACATGGGAGA CATGGTGGAC AGACTATTGG CAAGCCACCT GGATCCCTGA
3781 GTGGGAGTTT GTTAATACCC CTCCCCTAGT AAAATTATGG TACCAACTAG AAAAAGATCC
3841 CATAGCAGGA GTAGAAACTT TCTATGTAGA TGGAGCAACT AATAGGGAAG CTAAAATAGG
3901 AAAAGCAGGG TATGTTACTG ACAGAGGAAG GCAGAAAATT GTTACTCTAA CTAACACAAC
3961 AAATCAGAAG ACTGAGTTAC AAGCAATTCA GCTAGCTCTG CAGGATTCAG GATCAGAAGT
4021 AAACATAGTA ACAGACTCAC AGTATGCATT AGGAATCATT CAAGCACAAC CAGATAAGAG
4081 TGACTCAGAG ATATTTAACC AAATAATAGA ACAGTTAATA AACAAGGAAA GAATCTACCT
4141 GTCATGGGTA CCAGCACATA AAGGAATTGG GGGAAATGAA CAAGTAGATA AATTAGTAAG
4201 TAAGGGAATT AGGAAAGTGT TGTTTCTAGA TGGAATAGAT AAAGCTCAAG AAGAGCATGA
4261 AAGGTACCAC AGCAATTGGA GAGCAATGGC TAATGAGTTT AATCTGCCAC CCATAGTAGC
4321 AAAAGAAATA GTAGCTAGCT GTGATAAATG TCAGCTAAAA GGGGAAGCCA TACATGGACA
4381 AGTCGACTGT AGTCCAGGGA TATGGCAATT AGATTGTACC CATTTAGAGG GAAAAATCAT
4441 CCTGGTAGCA GTCCATGTAG CTAGTGGCTA CATGGAAGCA GAGGTTATCC CAGCAGAAAC
4501 AGGACAAGAA ACAGCATATT TTATATTAAA ATTAGCAGGA AGATGGCCAG TCAAAGTAAT
4561 ACATACAGAC AATGGCAGTA ATTTTACCAG TACTGCAGTT AAGGCAGCCT GTTGGTGGGC
4621 AGGTATCCAA CAGGAATTTG GAATTCCCTA CAATCCCCAA AGTCAGGGAG TGGTAGAATC
4681 CATGAATAAA GAATTAAAGA AAATAATAGG ACAAGTAAGA GATCAAGCTG AGCACCTTAA
4741 GACAGCAGTA CAAATGGCAG TATTCATTCA CAATTTTAAA AGAAAAGGGG GAATTGGGGG
4801 GTACAGTGCA GGGGAAAGAA TAATAGACAT AATAGCAACA GACATACAAA CTAAAGAATT
4861 ACAAAAACAA ATTATAAGAA TTCAAAATTT TCGGGTTTAT TACAGAGACA GCAGAGACCC
4921 TATTTGGAAA GGACCAGCCG AACTACTCTG GAAAGGTGAA GGGGTAGTAG TAATAGAAGA
4981 TAAAGGTGAC ATAAAGGTAG TACCAAGGAG GAAAGCAAAA ATCATTAGAG ATTATGGAAA
5041 ACAGATGGCA GGTGCTGATT GTGTGGCAGG TGGACAGGAT GAAGATTAGA GCATGGAATA
5101 GTTTAGTAAA GCACCATATG TATATATCAA GGAGAGCTAG TGGATGGGTC TACAGACATC
5161 ATTTTGAAAG CAGACATCCA AAAGTAAGTT CAGAAGTACA TATCCCATTA GGGGATGCTA
5221 GATTAGTAAT AAAAACATAT TGGGGTTTGC AGACAGGAGA AAGAGATTGG CATTTGGGTC
5281 ATGGAGTCTC CATAGAATGG AGACTGAGAG AATACAGCAC ACAAGTAGAC CCTGACCTGG
5341 CAGACCAGCT AATTCACATG CATTATTTTG ATTGTTTTAC AGAATCTGCC ATAAGACAAG
5401 CCATATTAGG ACACATAGTT TTTCCTAGGT GTGACTATCA AGCAGGACAT AAGAAGGTAG
5461 GATCTCTGCA ATACTTGGCA CTGACAGCAT TGATAAAACC AAAAAAGAGA AAGCCACCTC
5521 TGCCTAGTGT TAGAAAATTA GTAGAGGATA GATGGAACGA CCCCCAGAAG ACCAGGGGCC
5581 GCAGAGGGAA CCATACAATG AATGGACACT AGAGATTCTA GAAGAACTCA AGCAGGAAGC
5641 TGTCAGACAC TTTCCTAGAC CATGGCTCCA TAGCTTAGGA CAATATATCT ATGAAACCTA
5701 TGGGGATACT TGGACGGGAG TTGAAGCTAT AATAAGAGTA CTGCAACAAC TACTGTTCAT
5761 TCATTTCAGA ATTGGATGCC AACATAGCAG AATAGGCATC TTGCGACAGA GAAGAGCAAG
5821 AAATGGAGCC AGTAGATCCT AAACTAAAGC CCTGGAACCA TCCAGGAAGC CAACCTAAAA
5881 CAGCTTGTAA TAATTGCTTT TGCAAACACT GTAGCTATCA TTGTCTAGTT TGCTTTCAGA
5941 CAAAAGGTTT AGGCATTTCC TATGGCAGGA AGAAGCGGAG ACAGCGACGA AGCGCTCCTC
6001 CAAGTGGTGA AGATCATCAA AATCCTCTAT CAAAGCAGTA AGTACACATA GTAGATGTAA
6061 TGGTAAGTTT AAGTTTATTT AAAGGAGTAG ATTATAGATT AGGAGTAGGA GCATTGATAG
6121 TAGCACTAAT CATAGCAATA ATAGTGTGGA CCATAGCATA TATAGAATAT AGGAAATTGG
6181 TAAGACAAAA GAAAATAGAC TGGTTAATTA AAAGAATTAG GGAAAGAGCA GAAGACAGTG
6241 GCAATGAGAG TGATGGGGAC ACAGAAGAAT TGTCAACAAT GGTGGATATG GGGCATCTTA
6301 GGCTTCTGGA TGCTAATGAT TTGTAACACG GAGGACTTGT GGGTCACAGT CTACTATGGG
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FIGURE 1C

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6361 GTACCTGTGT GGAGAGAAGC AAAAACTACT CTATTCTGTG CATCAGATGC TAAAGCATAT
6421 GAGACAGAAG TGCATAATGT CTGGGCTACA CATGCTTGTG TACCCACAGA CCCCAACCCA
6481 CAAGAAATAG TTTTGGGAAA TGTAACAGAA AATTTTAATA TGTGGAAAAA TAACATGGCA
6541 GATCAGATGC ATGAGGATAT AATCAGTTTA TGGGATCAAA GCCTAAAGCC ATGTGTAAAG
6601 TTGACCCCAC TCTGTGTCAC TTTAAACTGT ACAGATACAA ATGTTACAGG TAATAGAACT
6661 GTTACAGGTA ATACAAATGA TACCAATATT GCAAATGCTA CATATAAGTA TGAAGAAATG
6721 AAAAATTGCT CTTTCAATGC AACCACAGAA TTAAGAGATA AGAAACATAA AGAGTATGCA
6781 CTCTTTTATA AACTTGATAT AGTACCACTT AATGAAAATA GTAACAACTT TACATATAGA
6841 TTAATAAATT GCAATACCTC AACCATAACA CAAGCCTGTC CAAAGGTCTC TTTTGACCCG
6901 ATTCCTATAC ATTACTGTGC TCCAGCTGAT TATGCGATTC TAAAGTGTAA TAATAAGACA
6961 TTCAATGGGA CAGGACCATG TTATAATGTC AGCACAGTAC AATGTACACA TGGAATTAAG
7021 CCAGTGGTAT CAACTCAACT ACTGTTAAAT GGTAGTCTAG CAGAAGAAGG GATAATAATT
7081 AGATCTGAAA ATTTGACAGA GAATACCAAA ACAATAATAG TACATCTTAA TGAATCTGTA
7141 GAGATTAATT GTACAAGGCC CAACAATAAT ACAAGGAAAA GTGTAAGGAT AGGACCAGGA
7201 CAAGCATTCT ATGCAACAAA TGACGTAATA GGAAACATAA GACAAGCACA TTGTAACATT
7261 AGTACAGATA GATGGAATAA AACTTTACAA CAGGTAATGA AAAAATTAGG AGAGCATTTC
7321 CCTAATAAAA CAATAAAATT TGAACCACAT GCAGGAGGGG ATCTAGAAAT TACAATGCAT
7381 AGCTTTAATT GTAGAGGAGA ATTTTTCTAT TGCAATACAT CAAACCTGTT TAATAGTACA
7441 TACTACCCTA AGAATGGTAC ATACAAATAC AATGGTAATT CAAGCTTACC CATCACACTC
7501 CAATGCAAAA TAAAACAAAT TGTACGCATG TGGCAAGGGG TAGGACAAGC AATGTATGCC
7561 CCTCCCATTG CAGGAAACAT AACATGTAGA TCAAACATCA CAGGAATACT ATTGACACGT
7621 GATGGGGGAT TTAACAACAC AAACAACGAC ACAGAGGAGA CATTCAGACC TGGAGGAGGA
7681 GATATGAGGG ATAACTGGAG AAGTGAATTA TATAAATATA AAGTGGTAGA AATTAAGCCA
7741 TTGGGAATAG CACCCACTAA GGCAAAAAGA AGAGTGGTGC AGAGAAAAAA AAGAGCAGTG
7801 GGAATAGGAG CTGTGTTCCT TGGGTTCTTG GGAGCAGCAG GAAGCACTAT GGGCGCAGCG
7861 TCAATAACGC TGACGGTACA GGCCAGACAA CTGTTGTCTG GTATAGTGCA ACAGCAAAGC
7921 AATTTGCTGA AGGCTATAGA GGCGCAACAG CATATGTTGC AACTCACAGT CTGGGGCATT
7981 AAGCAGCTCC AGGCGAGAGT CCTGGCTATA GAAAGATACC TAAAGGATCA ACAGCTCCTA
8041 GGGATTTGGG GCTGCTCTGG AAGACTCATC TGCACCACTG CTGTGCCTTG GAACTCCAGT
8101 TGGAGTAATA AATCTGAAGC AGATATTTGG GATAACATGA CTTGGATGCA GTGGGATAGA
8161 GAAATTAATA ATTACACAGA AACAATATTC AGGTTGCTTG AAGACTCGCA AAACCAGCAG
8221 GAAAAGAATG AAAAAGATTT ATTAGAATTG GACAAGTGGA ATAATCTGTG GAATTGGTTT
8281 GACATATCAA ACTGGCTGTG GTATATAAAA ATATTCATAA TGATAGTAGG AGGCTTGATA
8341 GGTTTAAGAA TAATTTTTGC TGTGCTCTCT ATAGTGAATA GAGTTAGGCA GGGATACTCA
8401 CCTTTGTCAT TTCAGACCCT TACCCCAAGC CCGAGGGGAC TCGACAGGCT CGGAGGAATC
8461 GAAGAAGAAG GTGGAGAGCA AGACAGAGAC AGATCCATAC GATTGGTGAG CGGATTCTTG
8521 TCGCTTGCCT GGGACGATCT GCGGAGCCTG TGCCTCTTCA GCTACCACCG CTTGAGAGAC
8581 TTCATATTAA TTGCAGTGAG GGCAGTGGAA CTTCTGGGAC ACAGCAGTCT CAGGGGACTA
8641 CAGAGGGGGT GGGAGATCCT TAAGTATCTG GGAAGTCTTG TGCAGTATTG GGGTCTAGAG
8701 CTAAAAAAGA GTGCTATTAG TCCGCTTGAT ACCATAGCAA TAGCAGTAGC TGAAGGAACA
8761 GATAGGATTA TAGAATTGGT ACAAAGAATT TGTAGAGCTA TCCTCAACAT ACCTAGGAGA
8821 ATAAGACAGG GCTTTGAAGC AGCTTTGCTA TAAAATGGGA GGCAAGTGGT CAAAACGCAG
8881 CATAGTTGGA TGGCCTGCAG TAAGAGAAAG AATGAGAAGA ACTGAGCCAG CAGCAGAGGG
8941 AGTAGGAGCA GCGTCTCAAG ACTTAGATAG ACATGGGGCA CTTACAAGCA GCAACACACC
9001 TGCTACTAAT GAAGCTTGTG CCTGGCTGCA AGCACAAGAG GAGGACGGAG ATGTAGGCTT
9061 TCCAGTCAGA CCTCAGGTAC CTTTAAGACC AATGACTTAT AAGAGTGCAG TAGATCTCAG
9121 CTTCTTTTTA AAAGAAAAGG GGGACTGGA AGGGTTAATT TACTCTAGGA AAAGGCAAGA
9181 AATCCTTGAT TTGTGGGTCT ATAACACACA AGGCTTCTTC CCTGATTGGC AAAACTACAC
9241 ATCGGGGCCA GGGGTCCGAT TCCCACTGAC CTTTGGATGG TGCTTCAAGC TAGTACCAGT
9301 TGACCCAAGG GAGGTGAAAG AGGCCAATGA AGGAGAAGAC AACTGTTTGC TACACCCTAT
9361 GAGCCAACAT GGAGCAGAGG ATGAAGATAG AGAAGTATTA AAGTGGAAGT TTGACAGCCT
9421 TCTAGCACAC AGACACATGG CCCGCGAGCT ACATCCGGAG TATTACAAAG ACTGCTGACA
```

FIGURE 1D

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9481 CAGAAGGGAC TTTCCGCCTG GGACTTTCCA CTGGGGCGTT CCGGGAGGTG TGGTCTGGGC
9541 GGGACTTGGG AGTGGTCACC CTCAGATGCT GCATATAAGC AGCTGCTTTT CGCTTGTACT
9601 GGGTCTCTCT CGGTAGACCA GATCTGAGCC TGGGAGCTCT CTGGCTATCT AGGGAACCCA
9661 CTGCTTAGGC CTCAATAAAG CTTGCCTTGA GTGCTCTAAG TAGTGTGTGC CCATCTGTTG
9721 TGTGACTCTG GTAACTAGAG ATCCCTCAGA CCCTTTGTGG TAGTGTGGAA AATCTCTAGC
9781 A
```

Figure 2A

↓ : indicates the regions for β-sheet and V1/V2 loop deletions

*: is the N-linked glycosylation sites for subtype C TV1 and TV2. Possible mutation (N→ Q) or deletions can be performed.

```
                 1                                                50
     B-SF162    (1)  ----MDAMKRGLCC LL C AVF SP- AV K WVTVYYGVPV  ATTT
   C-TV1.8_2    (1)   VM TQ C Q   I-CNT D WVTVYYGVPV A TT
   C-TV1.8_5    (1)   M TQ C Q   I-CNT D WVTVYYGVPV A TT
  C-TV2.12-5/1  (1)   AR IL YRH  M-CNVKG WVTVYYGVPV A TT
        C-MJ4   (1)   K IP      C-- VMGN WVTVYYGVPV A TT
 IndiaC-93IN101 (1)   VR TL Q   ICNGGGN WVTVYYGVPV A TT
      A-Q2317   (1)   M I Q C HLLT  ILGT FC AV N WVTVYYGVPV ADTT
    D-92UG001   (1)   REIE YLCL   LLG TY VA KKWVTVYYGVPV ATTT
      E-cm235   (1)  ----MDAMKRGLCC LL C AVF SP- ASN N WVTVYYGVPV ADTT
    Consensus   (1)  MRV G   RN Q WWIWGILGFWMLM   S   E LWVTVYYGVPVWREAKTT

                 51                                     *         100
     B-SF162   (46)  L CASDAK   E HN WATHACVPTDPNP E LENVTE FNMW NM
   C-TV1.8_2   (50)   QM    D   I SLWDQSLKPCVKLTPLCVT L C DTNVTGNRTVTGNSTNNTN
   C-TV1.8_5   (50)  L CASDAK  E HN WATHACVPTDPNP E LGNVTE FNMW N MA
  C-TV2.12-5/1 (50)  L CASDAK  KE HN WATHACVPTDPNP E LGNVTE FNMW NDM
        C-MJ4  (49)  L CASDAK  AE HN WATHACVPTDPNP E ELKNVTE FNMWENDM
 IndiaC-93IN101(51)  LLCASDAK  RE HN WATHACVPTDPNP E LGNVTE FNMW NDM
      A-Q2317  (51)  L CASDAK  EKHN WATHACVPTDPNP E HLDNVTEKFNMW N M
    D-92UG001  (51)  L CASDAK  K E HN WATHACVPTDPNPRE ELENVTE FNMW N M
      E-cm235  (46)  L CASDAK   E HN WATHACVPTDPNP E HLENVTE FNMW N M
    Consensus  (51)  LFCASDAKAYETEVHNVWATHACVPTDPNPQEIVL NVTENFNMWKNNMV

                                        ↓      *    *    *  β2/V1V2/β3
                 101                            *     *        * *150
     B-SF162   (96)   QM  D I ISLWDQSLKPCVKLTPLCVTLHC LKNATN--------TKSS
   C-TV1.8_2  (100)   QM  D I SLWDQSLKPCVKLTPLCVT L C DTNVTGNRTVTGNSTNNTN
   C-TV1.8_5  (100)   QM  D I SLWDQSLKPCVKLTPLCVT L NC DTNVTGNRTVTGNTNDTNI
  C-TV2.12-5/1(100)   QM Q D I ISLWDQSLKPCVKLTPLCVTL NC ATVNYN-------NTS--
        C-MJ4  (99)   QM  D I ISLWDQSLKPCVKLTPLCVT L NCK VTSKDI----------NI
 IndiaC-93IN101(101)  QM  D ISLWDQSLKPCVKLTPLCVTLECR VSRNVS----------SY
      A-Q2317 (101)   QM TD I ISLWDQSLKPCVKLTPLCVTLHC VTSVNT------------
    D-92UG001 (101)   QM  D I ISLWDQSLKPCVKLTPLCVT L NC DARRNET-------RNNIT
      E-cm235  (96)   QM  D I ISLWDQSLKPCVKLTPLCVT L NC AKLTNV-----NNITSVS
    Consensus (101)  DQMHEDIISLWDQSLKPCVKLTPLCVTLNCTN

                 151        *    *                           200
     B-SF162  (138)  NWKEMDRG  KNCSFK T S N MQ YALFY LD V DN-----DN
   C-TV1.8_2 (150)  G GIYNI  M NCSF AT DR H YALFY LD V N---E SDNF
   C-TV1.8_5 (150)  ANATYKY M NCSF AT DR HK YALFY LD V N---E S NF
  C-TV2.12-5/1(141)  -------K M NCSF T DK NALFY LD V NR-K GN IN
        C-MJ4 (139)  T NAEMKA M NCSF T DK QK YALFY LD V TNDNASE A
 IndiaC-93IN101(141)  N YNGSV   KNCSF ATP DR Q M ALFYGLD V KKNSSE S
      A-Q2317 (139)  - G--DR G KNCSF T DR Q V LFY LD V E----N G
    D-92UG001 (144)  GMENNDQI KNCSF T K I DK QV ALFY LD VQ DNDTS S Y
      E-cm235 (141)  N IGNIT V KNCSF T DK Q V ALFY LD V ED---KTS
    Consensus (151)  T      EEMKNCSFNITTELRDKK.KEYALFYKLDIVPLN    N N S
```

Figure 2B

```
                        201        *       ↓                    *      * 250
         B-SF162    (183) SYRLINCNTSVILQACPKVSFDPIPIHYCAPAGYAILKCNDKKFNGSGPC
      C-TV1.8_2     (197) TYRLINCNTSTILQACPKVSFDPIPIHYCAPADYAILKCNNKTFNGTGPC
      C-TV1.8_5     (197) TYRLINCNTSTILQACPKVSFDPIPIHYCAPADYAILKCNNKTFNGTGPC
    C-TV2.12-5/1    (183) NYRLINCNTSAILQACPKVSFDPIPIHYCTPAGYAPLKCNDKFNGIGPC
         C-MJ4      (189) EYRLINC DTSTILQACPKVSFDPIPIHYCRPAGYVLKCNNKTFNGTGPC
   IndiaC-93IN101   (191) EYRLINCNTSAILQACPKVSFDPIPIHYCAPAGYAILKCNNKTFNGTGPC
       A-Q2317      (182) EYRLINCNTSAILQACPKVSFDPIPIHYCTPAGYAILKCKDEGFNGTGLC
      D-92UG001     (194) NYRLINCNTSAILQACPKVSFDPIPIHYCAPAGYAILKCRDKKFNGTGHC
       E-cm235      (188) EYRLINCNTSVIKQACPKVSFDPIPIHYCTPAGYAILKCNDKNFNGTGPC
      Consensus     (201) YRLINCNTS ITQACPKVSFDPIPIHYCAPAGYAILKCNNK FNGTGPC


                            *
                        251          *            *          *     300
         B-SF162    (233) TNVSTVQCTHGIRPVVSTQLLLNGSLAEEGVVIRSDNFTDNAKTIVQLK
      C-TV1.8_2     (247) YNVSIVQCTHGIKPVVSTQLLLNGSLAEEGEIIRSNNTENTKTIIVHLN
      C-TV1.8_5     (247) YNVSTVQCTHGIKPVVSTQLLLNGSLAEEGEIIRSNNTENTKTIIVHLN
    C-TV2.12-5/1    (233) DNVSIVQCTHGIKPVVSTQLLLNGSLAEKGEIIRSNNTNNVKTIVHLN
         C-MJ4      (239) NNVSTVQCTHGIKPVVSTQLLLNGSLAEKGEIIRSKNTDNVKTIVHLN
   IndiaC-93IN101   (241) NNVSTVQCTHGIKPVVSTQLLLNGSLAEGEIIIRSENTNNVKTIVHLN
       A-Q2317      (232) KNVSIVQCTHGIKPVVSTQLLLNGSLAEKNTIRSDNTNNAKIIIVQLV
      D-92UG001     (244) KNVSTVQCTHGIKPVVSTQLLLNGSLAEEEIIIRSDNTNAKTIVQLN
       E-cm235      (238) KNVSSVQCTHGIKPVVSTQLLLNGSLAEEEIIIRSENTNNAKTIVHLN
      Consensus     (251) NVSTVQCTHGIKPVVSTQLLLNGSLAEEEIIIRSENLTNN KTIIVHLN


                                                             *
                        301   *       *                      *     350
         B-SF162    (283) DSVEINCTRPN-NNTRKSITIGPGRAFYATGDIIGDIRQAHCNISGEKWN
      C-TV1.8_2     (297) QSVEINCTRPN-NNTRKSVRIGPGQAFYATNDWIGNIRQAHCNISTDKWN
      C-TV1.8_5     (297) QSVEINCTRPN-NNTRKSVRIGPGQAFYETNDWIGNIRQAHCNISTDKWN
    C-TV2.12-5/1    (283) ESVEIKCTRPGN-NNTRKSMRIGPGQAFYATGDIIGDIRQAHCNISKNEWN
         C-MJ4      (289) ESVEIECTRPG-NNNTRKSIRIGPGQAFYATGDIIGDIRAAHCNISESKWN
   IndiaC-93IN101   (291) QSVEIVCTRPN-NNTRKSIRIGPGQAFYATGDIIGDIRQAHCNISRDKWN
       A-Q2317      (282) QPVTIKCIRPN-NNTRKSIRIGPGQAFYATGDIIGDIRQAHCNISRSKWN
      D-92UG001     (294) ESVEINCTRPYYNQIRQRTSIGQGQALYTTR-WTGDIRKAHCNISKAGWN
       E-cm235      (288) KLVEINCTRPS-NNTRTSITIGPGQVFYRTGDIIGDIRKAHCEINGTKWN
      Consensus     (301) ESVEINCTRPN NNTRKSIRIGPGQAFYATGDIIGDIRQAHCNIS   KWN


                        351            *                        *400
         B-SF162    (332) NTLKQIVTKLQAQFGNKT-IVFKQSSGGDPEIVMHSFNCGGEFFYCNSTQ
      C-TV1.8_2     (346) KTLQQVMKKLGEHFPNKT-IQFKQHAGGDLEIMMHSFNCRGEFFYCNLGN
      C-TV1.8_5     (346) KTLQQVMKKLGEHFPNKT-IKFEPHAGGDLEIMMHSFNCRGEFFYCNTSN
    C-TV2.12-5/1    (332) THLQRVSQKLQELFPNSTGIKFAPHEGGDLEIITHFFNCGGEFFYCNSTD
         C-MJ4      (338) KILYRVSEKLKEHFPNKT-IQFDQPIGGDIEIITHSFNCRGEFFYCNTDK
   IndiaC-93IN101   (340) ELLQRVGKKLAEHFHNKT-IKFASSSGGDLEIITHSFNCRGEFFYCNSSG
       A-Q2317      (331) KTLQEVAEKLRTSFGNKT-IIFANSSGGDTEIITHSFNCGGEFFYCNISG
      D-92UG001     (343) KTLQQVAKKLGDLFNQTT-IIFKQSSGGDPEIITHSFNCGGEFFYCNTSK
       E-cm235      (337) EVLTQVTEKLKEHFNNKT-IIFQQPEGGDLEIMMHHFNCRGEFFYCNTTR
      Consensus     (351) KTLQQV KL EHF NKT I F P SGGDLEITTHSFNCRGEFFYCNTS
```

Figure 2C

```
                           *                          ↓  β20/β21    ↓50
                    401·         *        *
B-SF162        (381) LFNS  NN-----TIGPN   -TNG I  PCRIKQI  RWQE G A YA P
C-TV1.8_2      (395) LFN   HS---N   YKY GNSSSPI  QC IKQI  R WQ  GQATYA P
C-TV1.8_5      (395) LFN   YP---K   YKY GNSSLPI  QC IKQI  R WQ  GQA YA P
C-TV2.12-5/1   (382) LFN   SNGTCT   CMS  --NTERI   QC IKQI   WQE G A YA P
C-MJ4          (387) LFNG  NS-----TGDTS  ----S I  SC IKQI   WQ  G A YASP
IndiaC-93IN101 (389) LFNG  MPTYMP    ESNS---   I   CR IKQI   WQE G A YA P
A-Q2317        (380) LFN   YVNSTW  DST  -ESND  I  CR IKQI   WQRAGQA YA P
D-92UG001      (392) LFNSA  ND-STW IGNNNTGSDNE  I I  CR IKQI   WQ  G A YA P
E-cm235        (386) LFNN CIE---- N  MGGC---NG I IL C IKQI   WQ AGQA YA P
Consensus      (401) LFNSTY     NGT    N    N TITLPCRIKQIINMWQGVGRAMYAPP
```

```
                    451*       *              *  *                       500
B-SF162        (424) IRG IRCSSNITG LL  DGGKEI NT---TEIFRP GG M DNWRSELY
C-TV1.8_2      (442) I GN I CRSNITG LL  DGGFNT N ---TE FRP GG M DNWRSELY
C-TV1.8_5      (442) I GN I CRSNITG LL  DGGFN N DT-EE FRP GG M DNWRSELY
C-TV2.12-5/1   (430) I GN I CRSNITG LL  DGGDN  ET----E FRP GG M DNWRSELY
C-MJ4          (428) I GN I CKSNITG LL  DGGNET GI----EIFRP GG M DNWRSELY
IndiaC-93IN101 (436) I GN I CTSNITG LLVHDGGIKENDTENKTEIFRP GG M DNWRSELY
A-Q2317        (429) IPGVIKCESNITG LL  DGGKD NV  ----E FRP GG M DNWRSELY
D-92UG001      (441) IEGWINCASNITG LLV DGGGA DS  ---NE FRPQGG M DNWRSELY
E-cm235        (429) I GRINCVSNITG LL  DGGAI  T ----E FRP GGN  DNWRSELY
Consensus      (451) IAGNITC SNITGLLLTRDGG  NT N     ETFRPGGGDMRDNWRSELY
```

```
                    501                                               550
B-SF162        (471) KYKVVKIEPLG APT KRRVVQR KRA T GA   GFLGAAGSTMGARS
C-TV1.8_2      (489) KYKV I PLG APT KRRVVQR KRA   GA   GFLGAAGSTMGA S
C-TV1.8_5      (491) KYKV I PLG APT KRRVVQRKKRA   GA   GFLGAAGSTMGA S
C-TV2.12-5/1   (476) KYKVV I PLG APTA KRRVV R KRA   GA   GFLGAAGSTMGA S
C-MJ4          (474) KYKVV I PLG APT KRRVV R KRA TFGA   GFLGAAGSTMGA S
IndiaC-93IN101 (486) KYKV I PLG APTA KRRVV R KRA   GA   GFLGAAGSTMGA S
A-Q2317        (475) KYKVV I PLG APT KRRVV R KRA   GA   GFLGAAGSTMGATS
D-92UG001      (488) KYKV VKIEPLG APT KRRVV R KRA   GA   GFLGAAGSTMGA S
E-cm235        (475) KYKVVQIEPLG APT KRRVV R KRA   GA  IFGFLGAAGSTMGA S
Consensus      (501) KYKVVEIKPLGIAPTKAKRRVVEREKRAVGIGAVFLGFLGAAGSTMGAAS
```

```
                    551                                               600
B-SF162        (521)  TLT QARQLLSGIV  QNNLL AIEAQQH L LTVWGIKQLQ R LA E
C-TV1.8_2      (539)  TLT QARQLLSGIV  Q NLL AIEAQQH L LTVWGIKQLQ R LA E
C-TV1.8_5      (541)  TLT QARQLLSGIV  O NLL AIEAQQH L LTVWGIKQLQ R LA E
C-TV2.12-5/1   (526)  TLT QARQLLSGIV  Q NLL AIEAQQH L LTVWGIKQLQ R LA E
C-MJ4          (524)  TLT QARQLLSGIV  Q NLL AIEAQQH L LTVWGIKQLQTR LA E
IndiaC-93IN101 (536)  TLTAQARQLLSGIV  Q NLL AIEAQQH L LTVWGIKQLQTR LA E
A-Q2317        (525)  TLT QARQLLSGIV  QNNLL AIEAQQH LKLTVWGIKQLQ R LA E
D-92UG001      (538)  TLT QARQLLSGIVQHQNNLLMAIEAQQH L LTVWGIKQLQ R LA E
E-cm235        (525)  TLT QARQLLSGIV  Q NLL AIEAQQH L LTVWGIKQLQ R LA E
Consensus      (551) ITLTVQARQLLSGIVQQQSNLLRAIEAQQHLLQLTVWGIKQLQARVLAVE
```

Figure 2D

```
                      601                  *     *      .    *       650
    B-SF162   (571) RYLKDQQLLGIWGCSGKICTTAVPWNSSWSNKSLDQIWNNMTWMEWDRE
  C-TV1.8_2   (589) RYLKDQQLLGIWGCSGKICTTAVPWNSSWSNKSEKQIWDNNTWMQWDRE
  C-TV1.8_5   (591) RYLKDQQLLGIWGCSGKICTTAVPWNSSWSNKSEAQIWDNNTWMQWDRE
C-TV2.12-5/1   (576) RYLQDQQLLGIWGCSGKICTTNVLWNSSWSNKQSQIWDNNTWMQWDRE
      C-MJ4   (574) RYLKDQQLLGIWGCSGKICTTAVPWNSSWSNKQHIWDNNTWMQWDRE
IndiaC-93IN101 (586) RYLKDQQLLGIWGCSGKICTTAVPWNSSWSNKQSIWNNMTWMQWDRE
     A-Q2317   (575) RYLKDQQLLGIWGCSGKICTTNVPWNSSWSNKSLDIWNNMTWMQWDRE
   D-92UG001   (588) RYLQDQQLLGSWGCSGRHICTTTVPWNSSWSNKSIDDIWNNMTWMEWDRE
    E-cm235   (575) RYLKDQKFLGIWGCSGKICTTAVPWNSWSNKSYEQIWNNMTWMEWDRE
  Consensus   (601) RYLKDQQLLGIWGCSGKLICTTAVPWNSSWSNKS  DIWNNMTWMQWDRE


                      *
                      651                                          700
    B-SF162   (621) TDNYTNLIYTLLEESQNQQEKNEQELLELDKWASLWNWFDISKWNWYIKI
  C-TV1.8_2   (639) ISNYTGLIENLLEESQNQQEKNEKDLLELDKWNNLWNWFDISNWPWYIKI
  C-TV1.8_5   (641) TNNYTETILENLLEESQNQQEKNEKDLLELDKWNNLWNWFDISNWLWYIKI
C-TV2.12-5/1   (626) IENYTNTIERNLLDSQSQQEKNEKDLLALDSWNNLWNWFSINNWLWYIKI
      C-MJ4   (624) ISNYTDTIERNLLEESQNQQEKNEKDLLALDSWKTLWSWFDISNWLWYIKI
IndiaC-93IN101 (636) VSNYTNLIKSLLEESQNQQEKNEKDLLALDSWKNLWSWFDILWNWYIKI
     A-Q2317   (625) TNNYTQLIERLLEESQNQQEKNEKELLELDKWANLWSWFDISNWLWYIKI
   D-92UG001   (638) TDNYTGVIENLLEESQTQQEKNEQELLQLDKWASLWNWFSIKKWNWYIKI
    E-cm235   (625) VSNYTNQIERNLLTESQNQQEKNEKDLLELDKWASLWNWFDISKWLWYIKI
  Consensus   (651) ISNYTNLIYRLLEESQNQQEKNEKDLLELDKW  NLWNWFDISNWLWYIKI


                      701                     .                     750
    B-SF162   (671) FIMIVGGLVGLRIVFTVLSIVNRVRQGYSPLSFQTRFPAPRGDRPEGIE
  C-TV1.8_2   (689) FIMIVGGLIGLRIIFAVLSIVNRVRQGYSPLSFQTLTPSRGLDRIGGIE
  C-TV1.8_5   (691) FIMIVGGLIGLRIIFAVLSIVNRVRQGYSPLSFQTLTPSRGLDRIGGIE
C-TV2.12-5/1   (676) FIMIVGGLIGLRIIFAVLSIVNRVRQGYSPLSLQTLIPNLRGPDRIGGIE
      C-MJ4   (674) FIMIVGSLIGLRIIFAVLSIVNRVRQGYSPLSFQTLIPNFRGPDRIGGIE
IndiaC-93IN101 (686) FIMIVGGLIGLRIIFAVLSIVNRVRQGYSPLSFQTLILNLRGSDRIGRIE
     A-Q2317   (675) FIMIVGGLIGLRIIFAVLSIVNRVRQGYSPLSFQTHIPNFRGLDRPERIE
   D-92UG001   (688) FIMILGGLIGLRIIFTVLSIVNRVRQGYSPLSFQTMFLAPRGPDRPEIE
    E-cm235   (675) FIMIIGGLIGLRIIFAVLSIVNRVRQGYSPLSFQTPFHHQREHDRSERIE
  Consensus   (701) FIMIVGGLIGLRIIFAVLSIVNRVRQGYSPLSFQTLTP  PRGPDRLEGIE


                      751                                          800
    B-SF162   (721) EGGERDRDRSSPLVHGLLALIWDDLRSLCLFSYHRLRDLILIAARIVEL
  C-TV1.8_2   (739) EGGGEQDRDRSIRLVSGFLSLAWDDLRNLCLFSYHRLRDEILIAVRAVEL
  C-TV1.8_5   (741) EGGGEQDRDRSIRLVSGFLALAWDDLRSLCLFCYHRLRDEILIAVRAVEL
C-TV2.12-5/1   (726) EGGGEQDSSRSIRLVSGFMTLAWDDLRSLCLFCYHRLRDEILIVVRAVEL
      C-MJ4   (724) EGGGEQDKDRSIRLVNGSIALAWDDLRSLCLFSYHQLRDFILIVVRAVEL
 IndiaC-93IN101 (736) EGGGEQDKDRSIRLVNGFLALAWDDLRNLCLFSYHRLRDEISIARVVEL
     A-Q2317   (725) EGDGEQGRGRSIRLVSGFINLAWDDLRSLCLFSYHRLRDEILIAARTVEL
   D-92UG001   (738) EGGGEQGRGRSTRLVNGFSTLIWDDLRNLCLFSYHRLRDLIIATRIVEL
    E-cm235   (725) EGGGEQGRERSIRLVSGFLALAWDDLRSLCLFSYHRLRDEILIAARTVKL
  Consensus   (751) EEGGEQDRDRSIRLVSGFLALAWDDLRSLCLFSYHRLRDFILIAAR  VEL
```

Figure 2E

```
                        801                                                    850
      B-SF162   (771)  LGR-------[RGWH]KYWGNL[]YWIQELKNS[]F[A]A[]VA[]TD
    C-TV1.8_2   (789)  LGHS[][]Q[GWI]KYL[SL]QYW[]ELK[S][][]A[]TVA[]TD
    C-TV1.8_5   (791)  LGH[][]OR[GWHI]KYL[]L[QYW[]ELK[S][]P[][]A[]AVA[]TD
  C-TV2.12-5/1  (776)  LGHS[][RG]QR[GWGT]KYL[]L[]QYW[]ELK[S][N][][]TA[]VA[]TD
        C-MJ4   (774)  LG[][]C[]QR[GWE]KYLGSL[]QYWGLELK[]ST[S][D]T[A]A[]VA[]TD
  IndiaC-93IN101(786)  LGR[]S-------WH[]KYL[SL]QYW[]ELK[S][]LFD[]A[]VVA[]TD
       A-Q2317  (775)  LGHSS[RG]RL[GWE]KY[]WNL[]SYWGRELKISA[N][]T[]A[]AVAGWTD
     D-92UG001  (788)  LGR-------RGWE[]KY[]WNL[]QYWSQELKTS[]F NATA[]VA[]TD
       E-cm235  (775)  LG[]SS[]QR[GWH]KY[]NL[]LYW[]QELKIS[][]A[]AT[]IVAGWTD
    Consensus   (801)  LGRSSLRGL RGWEALKYLGSLLQYWGLELKKSAISLLDTIAIAVAEGTD


                        851                   879
      B-SF162   (814)  R[][]E[]AQR[]GR[]F[]H[]P[]RIRQG[]ER[]L[]
    C-TV1.8_2   (839)  R[][]E[]QR[]CR[][]N[]P[]RIRQG[]E[]L[]
    C-TV1.8_5   (841)  R[][]E[]QR[]CR[][]N[]P[]RIRQG[]E[]L[]
  C-TV2.12-5/1  (826)  R[]EF[]QN[]CR[]R[]P[]RIRQG[]E[]LQ
        C-MJ4   (824)  R[][]E[]QR[]WR[]C[]P[]RIRQG[]E[]LL
  IndiaC-93IN101(829)  R[]E[]YQGFCR[]R[]PTRIRQG[]E[]LQ
       A-Q2317  (825)  R[]E[]AQR[]GR[][]H[]PVRIRQGLER[]LL
     D-92UG001  (831)  R[]E[]QR FFR[][]PTRIRQGLER[]LL
       E-cm235  (825)  R[]E[]AQGAWR[][]H[]P[]RIRQGLERTLL
    Consensus   (851)  RIIELVQRI RAILNIPRRIRQGFEAALL
```

Figure 3

Figure 4

Figure 5

Prebleed

2 wk post 4th

Log Geomean Titers

1000

100

10

1

B DNA + B prot

C DNA + B prot

B+C DNA + B prot

B+C DNA + C prot

B+C DNA & prot

B+C DNA & prot (1/2)

B+C DNA(1/2) + C prot

Immunization Groups
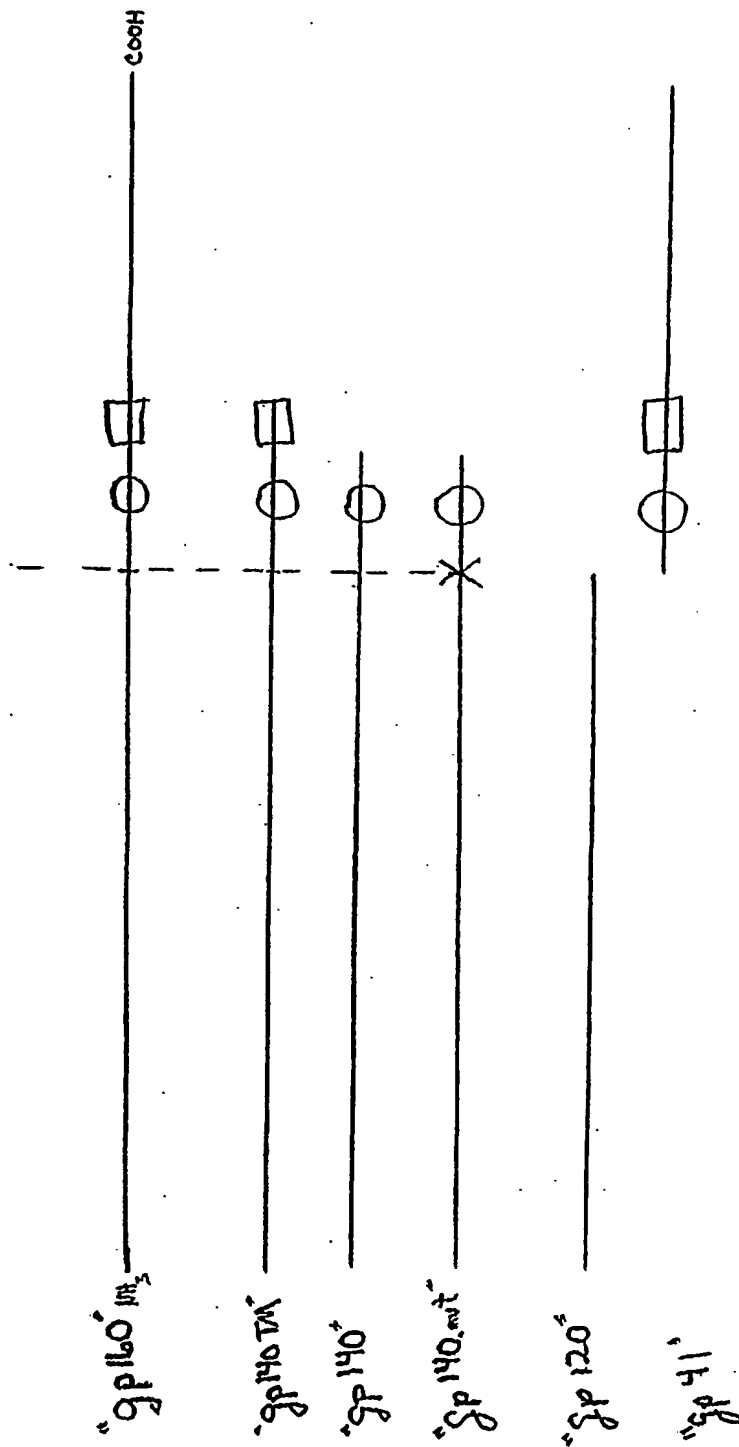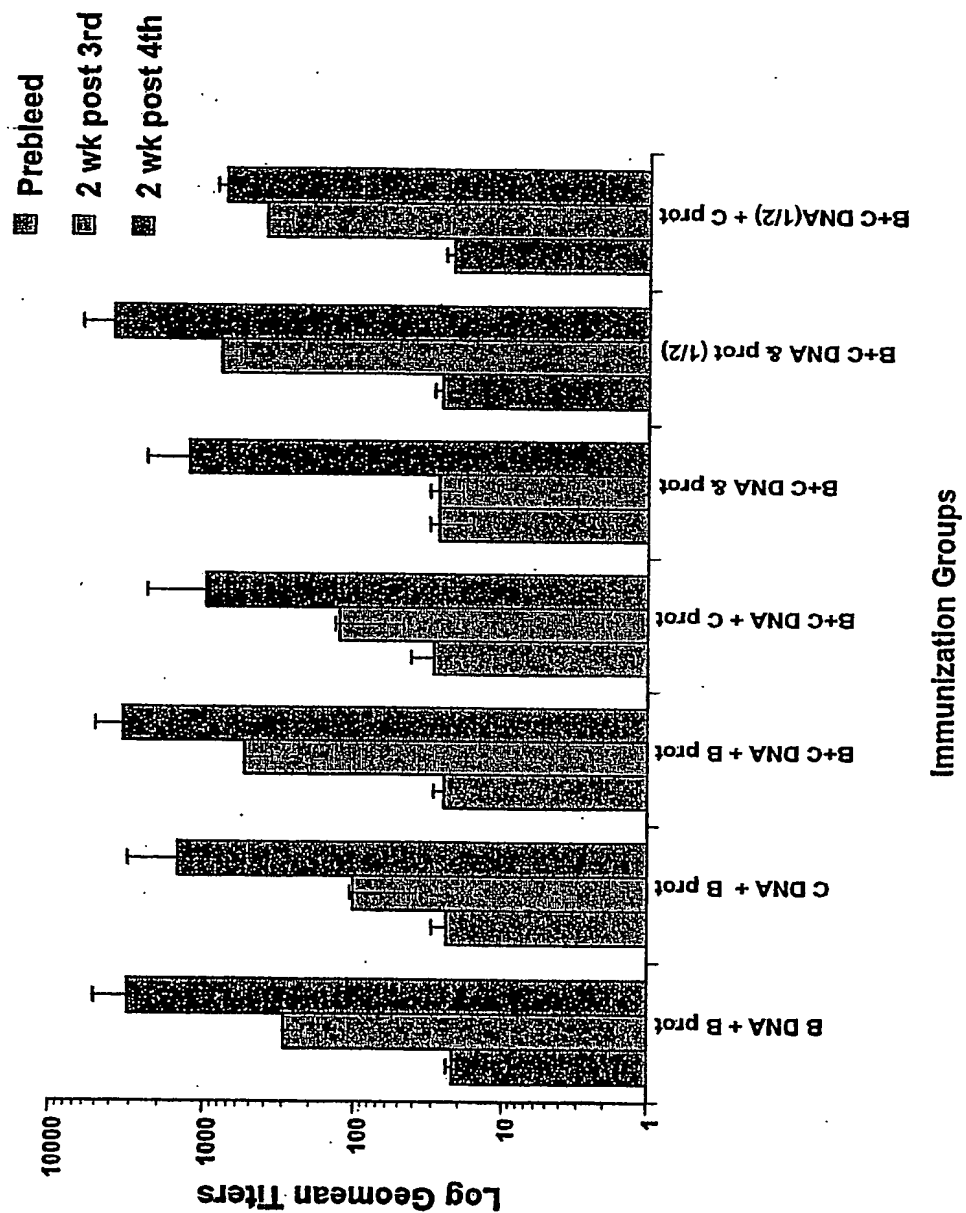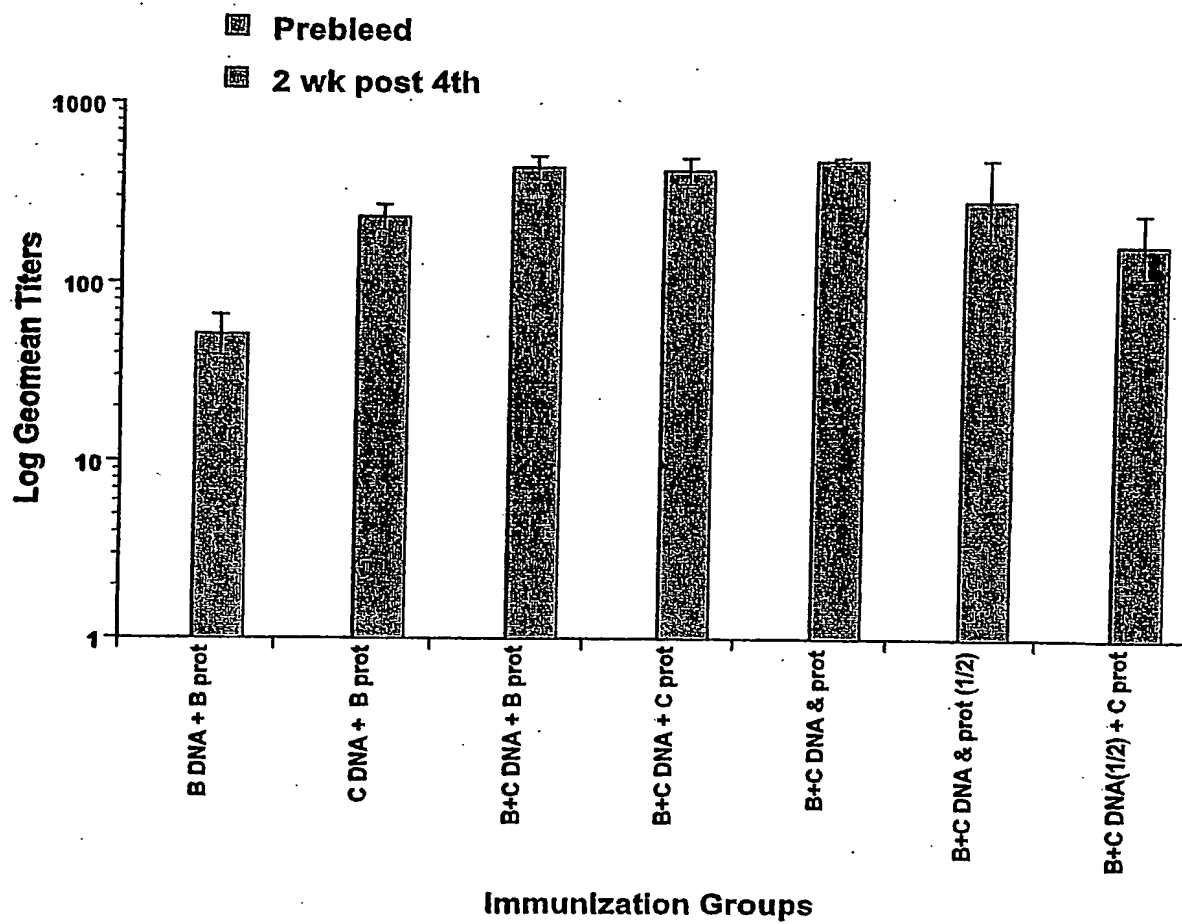
gp140.modSF162.delV2

```
gaattcgccaccatggatgcaatgaagagagggctctgctgtgtgctgctgctgtgtggagcagtc
ttcgtttcgcccagcgccgtggagaagctgtgggtgaccgtgtactacggcgtgcccgtgtggaag
gaggccaccaccaccctgttctgcgccagcgacgccaaggcctacgacaccgaggtgcacaacgtg
tgggccacccacgcctgcgtgcccaccgaccccaacccccaggagatcgtgctggagaacgtgacc
gagaacttcaacatgtggaagaacaacatggtggagcagatgcacgaggacatcatcagcctgtgg
gaccagagcctgaagccctgcgtgaagctgacccccctgtgcgtgaccctgcactgcaccaacctg
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gccaccggcgacatcatcggcgacatccgccaggcccactgcaacatcagcggcgagaagtggaac
aacaccctgaagcagatcgtgaccaagctgcaggcccagttcggcaacaagaccatcgtgttcaag
cagagcagcggcggcgaccccgagatcgtgatgcacagcttcaactgcggcggcgagttcttctac
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accatcacccctgccctgccgcatcaagcagatcatcaaccgctggcaggaggtgggcaaggccatg
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gagaagaacgagcaggagctgctggagctggacaagtgggccagcctgtggaactggttcgacatc
agcaagtggctgtggtacatctaactcgag
```

<div align="center">

Figure 6

</div>

gp140.mut7.modSF162.delV2

```
gaattcgccaccatggatgcaatgaagagagggctctgctgtgtgctgctgctgtgtggagcagtc
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atccgccccgtggtgagcacccagctgctgctgaacggcagcctggccgaggagggcgtggtgatc
cgcagcgagaacttcaccgacaacgccaagaccatcatcgtgcagctgaaggagagcgtggagatc
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gccaccggcgacatcatcggcgacatccgccaggcccactgcaacatcagcggcgagaagtggaac
aacaccctgaagcagatcgtgaccaagctgcaggcccagttcggcaacaagaccatcgtgttcaag
cagagcagcggcggcgacccccgagatcgtgatgcacagcttcaactgcggcggcgagttcttctac
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gagaagaacgagcaggagctgctggagctggacaagtgggccagcctgtggaactggttcgacatc
agcaagtggctgtggtacatctaactcgag
```

Figure 7

gp140mod.TV1.delV2

```
   1 gaattcatgc gcgtgatggg cacccagaag aactgccagc agtggtggat ctggggcatc
  61 ctgggcttct ggatgctgat gatctgcaac acggaggacc tgtgggtgac cgtgtactac
 121 ggcgtgcccg tgtggcgcga cgccaagacc accctgttct gcgccagcga cgccaaggcc
 181 tacgagaccg aggtgcacaa cgtgtgggcc acccacgcct ggtgccccac cgaccccaac
 241 ccccaggaga tcgtgctggg caacgtgacc gagaacttca acatgtggaa gaacgacatg
 301 gccgaccaga tgcacgagga cgtgatcagc ctgtgggacc agagcctgaa gccctgcgtg
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 421 accgtgaccg gcaacagcac caacaacacc aacggcaccg gcatctacaa catcgaggag
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 541 atcacccagg cctgccccaa ggtgagcttc gaccccatcc ccatccacta ctgcgcccc
 601 gccggctacg ccatcctgaa gtgcaacaac aagaccttca acggcacggg ccctgctac
 661 aacgtgagca ccgtgcagtg cacccacggc atcaagcccg tggtgagcac ccagctgctg
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 901 gtgatcggca acatccgcca ggcccactgc aacatcagca ccgaccgctg gaacaagacc
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1021 ccccacgccg gcggcgacct ggagatcacc atgcacagct tcaactgccg cggcgagttc
1081 ttctactgca acaccagcaa cctgttcaac agcacctacc acagcaacaa cggcacctac
1141 aagtacaacg gcaacagcag cagccccatc accctgcagt gcaagatcaa gcagatcgtg
1201 cgcatgtggc agggcgtggg ccaggccacc tacgcccccc ccatcgccgg caacatcacc
1261 tgccgcagca acatcaccgg catcctgctg acccgcgacg gcggcttcaa caccaccaac
1321 aacaccgaga ccttccgccc cggcggcggc gacatgcgcg acaactggcg cagcgagctg
1381 tacaagtaca aggtggtgga gatcaagccc ctgggcatcg cccccaccaa ggccaagcgc
1441 cgcgtggtgc agcgcgagaa gcgcgccgtg ggcatcggcg ccgtgttcct gggcttcctg
1501 ggcgccgccg gcagcaccat gggcgccgcc agcatcaccc tgaccgtgca ggcccgccag
1561 ctgctgagcg gcatcgtgca gcagcagagc aacctgctga ggccatcga ggcccagcag
1621 cacatgctgc agctgaccgt gtggggcatc aagcagctgc aggcccgcgt gctggccatc
1681 gagcgctacc tgaaggacca gcagctgctg ggcatctggg gctgcagcgg ccgcctgatc
1741 tgcaccaccg ccgtgccctg gaacagcagc tggagcaaca gagcgagaa ggacatctgg
1801 gacaacatga cctggatgca gtgggaccgc gagatcagca actacaccgg cctgatctac
1861 aacctgctgg aggacagcca gaaccagcag gagaagaacg agaaggacct gctggagctg
1921 gacaagtgga caacctgtg gaactggttc gacatcagca actggccctg gtacatctaa
1981 ctcgag
```

Figure 8

gp140mod.TV1.mut7.delV2

```
   1 gaattcatgc gcgtgatggg cacccagaag aactgccagc agtggtggat ctggggcatc
  61 ctgggcttct ggatgctgat gatctgcaac acggaggacc tgtgggtgac cgtgtactac
 121 ggcgtgcccg tgtggcgcga cgccaagacc accctgttct gcgccagcga cgccaaggcc
 181 tacgagaccg aggtgcacaa cgtgtgggcc acccacgcct gcgtgcccac cgaccccaac
 241 cccaggagaa tcgtgctggg caacgtgacc gagaacttca acatgtggaa gaacgacatg
 301 gccgaccaga tgcacgagga cgtgatcagc ctgtgggacc agagcctgaa gccctgcgtg
 361 aagctgaccc ccctgtgcgt gaccctgaac tgcaccgaca ccaacgtgac cggcaaccgc
 421 accgtgaccg gcaacagcac caacaacacc aacggcaccg gcatctacaa catcgaggag
 481 atgaagaact gcagcttcaa cgccggcgcc ggccgcctga tcaactgcaa caccagcacc
 541 atcacccagg cctgccccaa ggtgagcttc gacccccatcc ccatccacta ctgcgccccc
 601 gccggctacg ccatcctgaa gtgcaacaac aagaccttca acggcaccgg ccctgctac
 661 aacgtgagca ccgtgcagtg cacccacggc atcaagcccg tggtgagcac ccagctgctg
 721 ctgaacggca gcctggccga ggagggcatc atcatccgca gcgagaacct gaccgagaac
 781 accaagacca tcatcgtgca cctgaacgag agcgtggaga tcaactgcac ccgcccccaac
 841 aacaacaccc gcaagagcgt gcgcatcggc cccggccagg ccttctacgc caccaacgac
 901 gtgatcggca acatccgcca ggcccactgc aacatcagca ccgaccgctg gaacaagacc
 961 ctgcagcagg tgatgaagaa gctgggcgag cacttcccca acaagaccat ccagttcaag
1021 cccccacgccg gcggcgacct ggagatcacc atgcacagct tcaactgccg cggcgagttc
1081 ttctactgca acaccagcaa cctgttcaac agcacctacc acagcaacaa cggcacctac
1141 aagtacaacg gcaacagcag cagccccatc accctgcagt gcaagatcaa gcagatcgtg
1201 cgcatgtggc agggcgtggg ccaggccacc tacgcccccc ccatcgccgg caacatcacc
1261 tgccgcagca acatcaccgg catcctgctg accccgcgacg gcggcttcaa caccaccaac
1321 aacaccgaga ccttccgccc cggcggcggc gacatgcgcg acaactggcg cagcgagctg
1381 tacaagtaca aggtggtgga gatcaagccc ctgggcatcg cccccaccaa ggccatcagc
1441 agcgtggtgc agagcgagaa gagcgccgtg ggcatcggcg ccgtgttcct gggcttcctg
1501 ggcgccgccg gcagcaccat gggcgccgcc agcatcaccc tgaccgtgca ggccggccag
1561 ctgctgagcg gcatcgtgca gcagcagagc aacctgctga ggccatcga ggccagcag
1621 cacatgctgc agctgaccgt gtggggcatc aagcagctgc aggcccgcgt gctggccatc
1681 gagcgctacc tgaaggacca gcagctgctg ggcatctggg gctgcagcgg ccgcctgatc
1741 tgcaccaccg ccgtgccctg gaacagcagc tggagcaaca gagcgagaa ggacatctgg
1801 gacaacatga cctggatgca gtgggaccgc gagatcagca actacaccgg cctgatctac
1861 aacctgctgg aggacagcca gaaccagcag gagaagaacg agaaggacct gctggagctg
1921 gacaagtgga caacctgtg gaactggttc gacatcagca ctggccctg gtacatctaa
1981 ctcgag
```

Figure 9

FIGURE 10
gp160mod.Q23-17

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   1 ATGCGCGTGA TGGGCATCCA GCGCAACTGC CAGCACCTGC TGACCTGGGG CATCATGATC
  61 CTGGGCACCA TCATCTTCTG CAGCGCCGTG GAGAACCTGT GGGTGACCGT GTACTACGGC
 121 GTGCCCGTGT GGCGCGACGC CGACACCACC CTGTTCTGCG CCAGCGACGC CAAGGCCTAC
 181 GAGACCGAGA AGCACAACGT GTGGGCCACC CACGCCTGCG TGCCCACCGA CCCCAACCCC
 241 CAGGAGATCC ACCTGGACAA CGTGACCGAG AAGTTCAACA TGTGGAAGAA CAACATGGTG
 301 GAGCAGATGC ACACCGACAT CATCAGCCTG TGGGACCAGA GCCTGAAGCC CTGCGTGAAG
 361 CTGACCCCCC TGTGCGTGAC CCTGCACTGC ACCAACGTGA CCAGCGTGAA CACCACCGGC
 421 GACCGCGAGG GCCTGAAGAA CTGCAGCTTC AACATGACCA CCGAGCTGCG CGACAAGCGC
 481 CAGAAGGTGT ACAGCCTGTT CTACCGCCTG GACATCGTGC CCATCAACGA GAACCAGGGC
 541 AGCGAGTACC GCCTGATCAA CTGCAACACC AGCGCCATCA CCCAGGCCTG CCCCAAGGTG
 601 AGCTTCGAGC CCATCCCCAT CCACTACTGC ACCCCCGCCG GCTTCGCCAT CCTGAAGTGC
 661 AAGGACGAGG GCTTCAACGG CACCGGCCTG TGCAAGAACG TGAGCACCGT GCAGTGCACC
 721 CACGGCATCA GCCCGTGGT GAGCACCCAG CTGCTGCTGA CGGCAGCCT GGCCGAGAAG
 781 AACATCACCA TCCGCAGCGA GAACATCACC AACAACGCCA AGATCATCAT CGTGCAGCTG
 841 GTGCAGCCCG TGACCATCAA GTGCATCCGC CCCAACAACA ACACCCGCAA GAGCATCCGC
 901 ATCGGCCCCG GCCAGGCCTT CTACGCCACC GGCGACATCA TCGGCGACAT CCGCCAGGCC
 961 CACTGCAACG TGACCCGCAG CCGCTGGAAC AAGACCCTGC AGGAGGTGGC CGAGAAGCTG
1021 CGCACCTACT CGGCAACAA GACCATCATC TTCGCCAACA GCAGCGGCGG CGACCTGGAG
1081 ATCACCACCC ACAGCTTCAA CTGCGGCGGC GAGTTCTTCT ACTGCAACAC CAGCGGCCTG
1141 TTCAACAGCA CCTGGTACGT GAACAGCACC TGGAACGACA CCGACAGCAC CCAGGAGAGC
1201 AACGACACCA TCACCCTGCC CTGCCGCATC AAGCAGATCA TCAACATGTG GCAGCGCGCC
1261 GGCCAGGCCA TGTACGCCCC CCCCATCCCC GGCGTGATCA AGTGCGAGAG CAACATCACC
1321 GGCCTGCTGC TGACCCGCGA CGGCGGCAAG GACAACAACG TGAACGAGAC CTTCCGCCCC
1381 GGCGGCGGCG ACATGCGCGA CAACTGGCGC AGCGAGCTGT ACAAGTACAA GGTGGTGGAG
1441 ATCGAGCCCC TGGGCGTGGC CCCCACCCGC GCCAAGCGCC GCGTGGTGGA GCGCGAGAAG
1501 CGCGCCGTGG GCATCGGCGC CGTGTTCCTG GGCTTCCTGG GCGCCGCCGG CAGCACCATG
1561 GGCGCCACCA GCATCACCCT GACCGTGCAG GCCCGCCAGC TGCTGAGCGG CATCGTGCAG
1621 CAGCAGAACA ACCTGCTGCG CGCCATCGAG GCCCAGCAGC ACCTGCTGAA GCTGACCGTG
1681 TGGGGCATCA AGCAGCTGCA GGCCCGCGTG CTGGCCGTGG AGCGCTACCT GCGCGACCAG
1741 CAGCTGCTGG GCATCTGGGG CTGCAGCGGC AAGCTGATCT GCACCACCAA CGTGCCCTGG
1801 AACAGCAGCT GGAGCAACAA GAGCCTGGAC GAGATCTGGA ACAACATGAC CTGGCTGCAG
1861 TGGGACAAGG AGATCAACAA CTACACCCAG CTGATCTACC GCCTGATCGA GGAGAGCCAG
1921 AACCAGCAGG AGAAGAACGA GAAGGAGCTG CTGGAGCTGG ACAAGTGGGC CAACCTGTGG
1981 AGCTGGTTCG ACATCAGCAA CTGGCTGTGG TACATCAAGA TCTTCATCAT CATCGTGGGC
2041 GGCCTGATCG GCCTGCGCAT CGTGTTCGCC GTGCTGAGCG TGATCAACCG CGTGCGCCAG
2101 GGCTACAGCC CCCTGAGCTT CCAGACCCAC ACCCCCAACC CCCGCGGCCT GGACCGCCCC
2161 GAGCGCATCG AGGAGGAGGA CGGCGAGCAG GGCCGCGGCC GCAGCATCCG CCTGGTGAGC
2221 GGCTTCCTGG CCCTGGCCTG GGACGACCTG CGCAGCCTGT GCCTGTTCAG CTACCACCGC
2281 CTGCGCGACT TCATCCTGAT CGCCGCCCGC ACCGTGGAGC TGCTGGGCCA CAGCAGCCTG
2341 AAGGGCCTGC GCCTGGGCTG GGAGGGCATC AAGTACCTGT GGAACCTGCT GAGCTACTGG
2401 GGCCGCGAGC TGAAGATCAG CGCCATCAAC CTGGTGGACA CCATCGCCAT CGCCGTGGCC
2461 GGCTGGACCG ACCGCGTGAT CGAGATCGCC CAGCGCATCG GCCGCGCCAT CCTGCACATC
2521 CCCGTGCGCA TCCGCCAGGG CCTGGAGCGC GCCCTGCTGT AA
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FIGURE 11

gp160mod.98UA0116

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   1 ATGAAGGCCC GCGGCATGCA GCGCAACTAC CAGCACCTGT GGCGCTGGGG.CACCATGCTG
  61 TTCTGGATGA TCATCATGTG CAAGGCCGCC GAGAACCTGT GGGTGACCGT GTACTACGGC
 121 GTGCCCGTGT GGCGCGACGC CGAGACCACC CTGTTCTGCG CCAGCGACGC CAAGGCCTAC
 181 GACAAGGAGG TGCACAACGT GTGGGCCACC CACGCCTGCG TGCCCACCGA CCCCGACCCC
 241 CAGGAGATCA TCCTGGAGAA CGTGACCGAG AAGTTCAACA TGTGGAAGAA CAACATGGTG
 301 GAGCAGATGC AGACCGACAT CATCAGCCTG TGGGACCAGA GCCTGAAGCC CTGCGTGAAG
 361 CTGACCCCCC TGTGCGTGAC CCTGAACTGC GCCGGCCCCA GCAGCAACAA CAGCAACGTG
 421 AACAGCAACA GCAACGACAA CTGGAGCGAG GAGATGAAGA ACTGCAGCTT CAACATGACC
 481 ACCGAGCTGC GCGACAAGCG CAAGACCGTG CACAGCCTGT TCTACAAGCT GGACATCGTG
 541 AGCACCGGCA.GCAACGACAG CCGCCAGTAC CGCCTGATCA ACTGCAACAC CAGCGCCATG
 601 ACCCAGGCCT GCCCCAAGGT GACCTTCGAG CCCATCCCCA TCCACTACTG CGCCCCCGCC
 661 GGCTTCGCCA TCCTGAAGTG CAAGGACACC AACTTCACCG GCACCGGCCC CTGCAAGGAC
 721 GTGAGCACCG TGCAGTGCAC CCACGGCACC AAGCCCGTGG TGAGCACCCA GCTGCTGCTG
 781 AACGGCAGCC TGGCCGAGAA GGAGGTGATG ATCCGCAGCG AGAACATCAC CGACAACGGC
 841 AAGATCATCA TCGTGCAGCT GACCGAGCCC GTGAACATCA CCCGCATCCG CCCCGGCGAG
 901 AACAAGCGCA CCAGCATCCG CATCGGCCCC GGCCAGACCT TCTACGCCAC CGGCGACGTG
 961 ATCGGCGACA TCCGCAAGGC CTACTGCAAC GTGAGCCGCG CCGCCTGGAA CAGCACCCTG
1021 CAGAAGATCA GCACCCAGCT GCGCCAGTAC TTCAACAACA GACCATCAT CTTCAAGAAC
1081 AGCAGCGGCG GCGACCTGGA GGTGACCACC CACAGCTTCA ACTGCGGCGG CGAGTTCTTC
1141 TACTGCAACA CCACCGACCT GTTCAACAGC ACCTGGAACG AGCACGGCCC CGTGACCAAC
1201 AGCACCATGG CCAACGGCAC CATCACCCTG CCCTGCCGCA TCAAGCAGAT CATCAACATG
1261 TGGCAGCGCG TGGGCCAGGC CATGTACGCC CCCCCCATCG AGGGCAACAT CCGCTGCGAG
1321 AGCAACATCA CCGGCCTGCT GCTGACCCGC GACGGCGGCA GCGGCGCCAA CAGCAGCAAG
1381 GAGACCTACC GCCCCATCGG CGGCAACATG CGCGACAACT GGCGCAGCGA GCTGTACAAG
1441 TACAAGGTGG TGAAGATCGA GCCCATCGGC GTGGCCCCCA CCAAGGCCAA GCGCCGCGTG
1501 GTGGAGCGCG AGAAGCGCGC CATCGGCCTG GGCGCCGCCT TCCTGGGCTT CCTGGGCGCC
1561 GCCGGCAGCA CCATGGGCGC CGCCAGCATG ACCCTGACCG TGCAGGCCCG CCAGCTGCTG
1621 AGCGGCATCG TGCAGCAGCA GAGCAACCTG CTGCGCGCCA TCGAGGCCCA GCAGCACCTG
1681 CTGAAGCTGA CCGTGTGGGG CATCAAGCAG CTGCAGGCCC GCGTGCTGGC CGTGGAGCGC
1741 TACCTGAAGG ACCAGCAGCT GCTGGGCATC TGGGGCTGCA GCGGCAAGCT GATCTGCACC
1801 ACCAACGTGC CCTGGAACAG CAGCTGGAGC AACAAGAGCC AGAGCGAGAT CTGGGGCAAC
1861 ATGACCTGGA TGCAGTGGGA CCGCGAGGTG ATCAACTACA CCAACATCAT CTACGACCTG
1921 ATCGAGGAGA GCCAGAACCA GCAGGAGAAG AACGAGCAGG ACCTGCTGGC CCTGGACAAG
1981 TGGGCCAGCC TGTGGAGCTG GTTCGACATC AGCAACTGGC TGTGGTACAT.CAAGATCTTC
2041 ATCATCATCG TGGGCGGCCT GATCGGCCTG CGCATCGTGT TCGCCGTGCT GAGCATCATC
2101 AACCGCGTCG GCCAGGGCTA CAGCCCCCTG AGCCTGCAGA CCCTGACCCC CCACCCCGAG
2161 GGCCCCGACC GCCCCGGCCG CATCAAGGAG GAGGGCGGCG AGCAGGACCG CGACCGCAGC
2221 ATCCGCCTGG TGAGCGGCTT CCTGGCCCTG GCCTGGGACG ACCTGCGCAG CCTGTGCCTG
2281 TTCAGCTACC GCCGCCTGCG CGACTTCATC AGCATCGCCG CCCGCACCGT GGAGCTGCTG
2341 GGCCGCAGCA GCCTGAAGGG CCTGCGCCTG GGCTGGGAGG CCTGAAGTA.CCTGGGCAAC
2401 CTGCTGGGCT ACCGCGGCCA GGAGCTGAAG AGCAGCGCCA TCAACCTGAT CGACACCATC
2461 GCCATCGCCG TGGCCGGCTG GACCGACCGC GTGATCGAGA TCGGCCAGCG CTTCTGCCGC
2521 GCCATCCGCA ACATCCCCCG CCGCATCCGC CAGGGCGCCG AGCGCGCCCT GCAGTAA
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FIGURE 12
gp160mod.SE8538

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   1 ATGCGCGTGA AGGGCATCCA GCGCAACAGC CAGCACCTGC TGCGCTGGGG CACCATGATC
  61 CTGGGCATGA TCATCATCTG CAGCACCGCC GACAAGCTGT GGGTGACCGT GTACTACGGC
 121 GTGCCCGTGT GGAAGGACGC CGAGACCACC CTGTTCTGCG CCAGCGACGC CAAGGCCTAC
 181 GACACCGAGG TGCACAACGT GTGGGCCACC CACGCCTGCG TGCCCACCGA CCCCAACCCC
 241 CAGGAGCTGC ACCTGGCCAA CGTGACCGAG GAGTTCAACA TGTGGAAGAA CAGCATGGTG
 301 GAGCAGATGC ACACCGACAT CATCAGCCTG TGGGACCAGA GCCTGATCCC CTGCGTGAAG
 361 CTGACCCCCC TGTGCGTGAC CCTGGAGTGC AACGACTACA ACTACAACGT GACCAACAGC
 421 AGCCACAGCT ACAACGTGAC CAACATGCAG GAGATGAAGA ACTGCAGCTT CAACGTGACC
 481 ACCGAGCTGC GCGACAAGCG CCAGAAGGTG ACCAGCCTGT CTACAAGCT GGACGTGGTG
 541 CCCATCGGCG GCAACGACAC CAACAGCACC CAGTACCGCC TGATCAACTG CAACACCAGC
 601 GCCATCACCC AGGCCTGCCC CAAGGTGACC TTCGAGCCCA TCCCCATCCA CTACTGCGCC
 661 CCCGCCGGCT TCGCCATCCT GAAGTGCCGC GACGAGAACT TCAACGGCAC CGGCCCCTGC
 721 AAGAACGTGA GCACCGTGCA GTGCACCCAC GGCATCAAGC CCGTGGTGAG CACCCAGCTG
 781 CTGCTGAACG GCAGCCTGGC CGAGGAGAAG GTGATGATCC GCAGCGAGAA CATCACCAAC
 841 AACGTGAAGA ACATCATCGT GCAGCTGAAG GAGCCCGTGG AGATCAACTG CACCCGCCCC
 901 GGCAACAACA CCCGCAAGAG CATCCGCATC GGCCCCGGCC AGGCCTTCTA CGCCACCGGC
 961 GAGGTGATCG GCGACATCCG CCAGGCCCAC TGCAACGTGA GCCGCGCCAA GTGGAACAAG
1021 ACCCTGCACG AGGTGGCCAA GCAGCTGCGC ACCTACTTCA CAACAAGGAC CATCATCTTC
1081 ACCAACAGCA GCGGCGGCGA CCTGGAGATC ACCACCCACA CCGTGAACTG CGGCGGCGAG
1141 TTCTTCTACT GCAACACCAG CGGCCTGTTC AACAGCACCT GGAGCAGCAA CGCCAGCGAG
1201 CCCATGAGCA CAGCACCGA GAGCAACGAC ACCATCACCC TGCAGTGCCG CATCCGCCAG
1261 ATCATCAACA TGTGGCAGCG CGCCGGCAAG GCCATCTACG CCCCCCCCAT CCCCGGCATC
1321 ATCAAGTGCG TGAGCAACAT CACCGGCCTG ATCCTGACCC GCGACGGCGG CAGCAACAAC
1381 AGCACCAACG AGACCTTCCG CCCCGGCGGC GGCGACATGC GCGACAACTG CGCGCAGCGAG
1441 CTGTACAAGT ACAAGGTGGT GAAGATCGAG CCCCTGGGCG TGGCCCCCAC CAAGGCCAAG
1501 CGCCGCGTGG TGGAGCGCGA GAAGCGCGCC ATCGGCATCG GCGCCGTGTT CATCGGCTTC
1561 CTGGGCGCCG CCGGCAGCAC CATGGGCGCC GCCAGCATCA CCCTGACCGT GCAGGCCCGC
1621 CAGCTGCTGA GCGGCATCGT GCAGCAGCAG AGCAACCTGC TGCGCGCCAT CGAGGCCCAG
1681 CAGCACCTGC TGAAGCTGAC CGTGTGGGGC ATCAAGCAGC TGCAGGCCCG CGTGCTGGCC
1741 GTGGAGCGCT ACCTGAAGGA CCAGCAGCTG CTGGGCATCT GGGGCTGCAG CGGCAAGCTG
1801 ATCTGCACCA CCAACGTGCC CTGGAACAGC AGCTGGAGCA ACAAGAGCCA GAGCGAGATC
1861 TGGGACAACA TGACCTGGCT GCAGTGGGAC AAGGAGATCA GCAACTACAC CCAGACCATC
1921 TACCGCCTGA TCGAGGAGAG CCAGAACCAG ACGAGCAGGA CCTGCTGGCC
1981 CTGGACAAGT GGGCCAGCCT GTGGAACTGG TTCGACATCA GCCGCTGGCT GTGGTACATC
2041 CGCATCTTCA TCATGATCGT GGGCGGCCTG ATCGGCCTGC GCATCGTGTT CGCCGTGCTG
2101 AGCGTGATCA ACCGCGTGCG CCAGGGCTAC AGCCCCCTGA GCTTCCAGAT CCACACCCCC
2161 AACCCCGGCG ACCTGGACCG CCCCGGCCGC ATCGAGGAGG AGGGCGGCGA GCAGGACCGC
2221 GGCCGCAGCA TCCGCCTGGT GAGCGGCTTC CTGGCCCTGG CCTGGGACGA CCTGCGCAGC
2281 CTGTGCCTGT TCAGCTACCA CCGCCTGCGC GACTTCATCC TGATCGCCGC CCGCACCGTG
2341 GAGCTGCTGG GCCAGCGCGG CTGGGAGGGC CTGAAGTACC TGTGGAACCT GCTGGTGTAC
2401 TGGATCCGCG AGCTGAAGAT CAGCGCCATC AGCCTGCTGG ACACCATCGC CATCGCCGTG
2461 GCCGGCTGGA CCGACCGCGT GATCGAGCTG GGCCAGCGCC TGTGCCGCGC CATCCTGCAC
2521 ATCCCCGTGC GCATCCGCCA GGGCTTCGAG CGCGCCCTGC TGTAA
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FIGURE 13

gp160mod.UG031

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   1 ATGCGCGTGC GCGGCATCCA GACCAGCTGG CAGAACCTGT GGCGCTGGGG CACCATGATC
  61 CTGGGCATGC TGATGATCTA CAGCGCCGCC GAGAACCTGT GGGTGACCGT GTACTACGGC
 121 GTGCCCGTGT GGAAGGACGC CGAGACCACC CTGTTCTGCG CCAGCGACGC CAAGGCCTAC
 181 GACACCGAGG TGCACAACGT GTGGGCCACC CACGCCTGCG TGCCCACCGA CCCCAACCCC
 241 CAGGAGATCC ACCTGGAGAA CGTGACCGAG GACTTCAACA TGTGGAAGAA CAACATGGTG
 301 GAGCAGATGC ACACCGACAT CATCAGCCTG TGGGACCAGA GCCTGAAGCC CTGCGTGGAG
 361 CTGACCCCCC TGTGCGTGAC CCTGGACTGC CTGAACGCCA CCCTGAACGC CACCGCCCCC
 421 AACGTGACCA ACGACATGGA GGGCGAGATG AAGAACTGCA GCTACAACAT CACCACCGAG
 481 CTGAAGGACA GAAGCAGCA GGTGTACAGC CTGTTCTACA AGCTGGACGT GGTGCAGATC
 541 AACGAGAAGA ACAAGACCAA CAAGTACCGC CTGATCAACT GCAACACCAG CGCCATCACC
 601 CAGGCCTGCC CCAAGGTGAG CTTCGAGCCC ATCCCCATCC ACTACTGCGC CCCCGCCGGC
 661 TTCGCCATCC TGAAGTGCAA GGACACCGAG TTCAACGGCA CCGGCCCCTG CAAGAACGTG
 721 AGCACCGTGC AGTGCACCCA CGGCATCCGC CCCGTGATCA GCACCCAGCT GCTGCTGAAC
 781 GGCAGCCTGG CCGAGGGCGG CATCCAGATC CGCAGCGAGA ACATCACCAA CAACGCCAAG
 841 ACCATCATCG TGCAGCTGGA CAAGGCCGTG AAGATCAACT GCACCCGCCC CAACAACAAC
 901 ACCCGCAAGA GCGTGCGCAT CGGCCCCGGC CAGGCCTTCT ACGCCACCGG CGACATCATC
 961 GGCGACATCC GCCAGGCCCA CTGCAACGTG AGCCGCGCCA AGTGGAACGA GACCCTGCGC
1021 GGCATCGCCA GAAGCTGAG CGAGCACTTC AAGAACAAGA TCATCATCTT CGAGAAGAGC
1081 AGCGGCGGCG ACATCGAGAT CACCACCCAC AGCTTCAACT GCGGCGGCGA GTTCTTCTAC
1141 TGCAACACCA GCGGCCTGTT CAACGGCACC TGGAAGCCCA CAGCACCGA GAGCAACAAC
1201 ACCACCCCCA ACGACACCAT CACCCTGACC TGCCGCATCA AGCAGATCAT CAACATGTGG
1261 CAGAAGGTGG GCCAGGCCAT GTACGCCCCC CCCATCCAGG GCGTGATCCG CTGCGAGAGC
1321 AACATCACCG GCCTGCTGCT GACCCGCGAC GGCGGCATCA ACAGCATCAA CGAGACCTTC
1381 CGCCCCGGCG GCGGCAACAT GCGCGACAAC TGGCGCAGCG AGCTGTACAA GTACAAGGTG
1441 GTGAAGATCG AGCCCCTGGG CGTGGCCCCC AGCCGCGCCA AGCGCCGCGT GGTGGAGCGC
1501 GAGAAGCGCG CCGTGGGCAT CGGCGCCGTG TTCCTGGGCT TCCTGGGCGC CGCCGGCAGC
1561 ACCATGGGCG CCGCCAGCAT CACCCTGACC GCCCAGGCCC GCCAGCTGCT GAGCGGCATC
1621 GTGCAGCAGC AGAGCAACCT GCTGCGCGCC ATCAAGGCCC AGCAGCACAT GCTGAAGCTG
1681 ACCGTGTGGG GCATCAAGCA GCTGCAGGCC CGCGTGCTGG CCGTGGAGCG CTACCTGAAG
1741 GACCAGCAGC TGCTGGGCAT CTGGGGCTGC AGCGGCAAGC TGATCTGCAC CACCAACGTG
1801 CCCTGGAACA GCAGCTGGAG CAACAAGAGC ATGAACGAGA TCTGGGACAA CATGACCTGG
1861 CTGCAGTGGG AGAAGGAGAT CAGCAACTAC ACCCAGCTGA TCTACAACCT GATCGAGGAG
1921 AGCCAGAACC AGCAGGAGAA GAACGAGCAG GACCTGCTGG CCCTGGACAA GTGGGCCAGC
1981 CTGTGGAACT GGTTCGACAT CAGCCGCTGG CTGTGGTACA TCAAGATCTT CATCATGATC
2041 GTGGGCGGCC TGATCGGCCT GCGCATCGTG TTCGCCGTGC TGAGCGTGAT CAACCGCGTG
2101 CGCCAGGGCT ACAGCCCCCT GAGCTTCCAG ATCCGCACCC CCAACCCCGA GGAGCCCGAC
2161 CGCCTGGGCC GCATCGGCGA GGAGGGCGGC GAGCAGGACC GCGACCGCAG CATCCGCCTG
2221 GTGAGCGGCT TCCTGGCCCT GGCCTGGGAC GACCTGCGCA GCCTGTGCCT GTTCAGCTAC
2281 CACCGCCTGC GCGACTTCAT CAGCATCGCC GCCCGCACCG TGGAGCTGCT GGGCCACAGC
2341 AGCCTGAAGG GCCTGCGCCT GGGCTGGGAG GGCCTGAAGT ACCTGTGGAA CCTGCTGCTG
2401 TACTGGGGCC TGGAGCTGAA GACCAGCGCC GTGAACCTGG TGGACACCAT CGCCATCGCC
2461 GTGGCCGGCT GGACCGACCG CGTGATCGAG ATCGGCCAGC GCATCTTCCG CGCCATCCTG
2521 AACATCCCCC GCCGCATCCG CCAGGGCCTG GAGCGCGGCC TGCTGTAA
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FIGURE 14

gp160mod.92UG001

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   1 ATGCGCGTGC GCGAGATCGA GCGCAACTAC CTGTGCCTGT GGCGCTGGGG CATCATGCTG
  61 CTGGGCATGC TGATGACCTA CAGCGTGGCC GAGAAGAAGT GGGTGACCGT GTACTACGGC
 121 GTGCCCGTGT GGAAGGAGGC CACCACCACC CTGTTCTGCG CCAGCGACGC CAAGAGCTAC
 181 AAGACCGAGG TGCACAACAT CTGGGCCACC CACGCCTGCG TGCCCACCGA CCCCAACCCC
 241 CGCGAGATCG AGCTGGAGAA CGTGACCGAG AACTTCAACA TGTGGAAGAA CAACATGGTG
 301 GAGCAGATGC ACGAGGACAT CATCAGCCTG TGGGACCAGA GCCTGAAGCC CTGCGTGAAG
 361 CTGACCCCCC TGTGCGTGAC CCTGAACTGC ACCGACGCCC GCCGCAACGA GACCCGCAAC
 421 AACATCACCG GCATGGAGAA CAACGACCAG ATCGAGATGA AGAACTGCAG CTTCAACATC
 481 ACCACCAAGC TGATCGACAA GAAGAAGCAG GTGCACGCCC TGTTCTACCG CCTGGACGTG
 541 GTGCAGATCG ACAACGACAC CAGCAACAGC AACTACAGCA ACTACCGCCT GATCAACTGC
 601 AACACCAGCG CCATCACCCA GGCCTGCCCC AAGGTGACCT TCGAGCCCAT CCCCATCCAC
 661 TACTGCGCCC CCGCCGGCTT CGCCATCCTG AAGTGCCGCG ACAAGAAGTT CAACGGCACC
 721 GGCCCCTGCA AGAACGTGAG CACCGTGCAG TGCACCCACG GCATCCGCCC CGTGGTGAGC
 781 ACCCAGCTGC TGCTGAACGG CAGCCTGGCC GAGGAGGAGA TCATCATCCG CAGCGAGAAC
 841 CTGACCAACA ACGCCAAGAC CCTGATCGTG CAGCTGAACG AGAGCGTGGA GATCAACTGC
 901 ACCCGCCCCT ACTACAACCA GATCCGCCAG CGCACCAGCA TCGGCCAGGG CCAGGCCCTG
 961 TACACCACCC GCGTGACCGG CGACATCCGC AAGGCCTACT GCAACATCAG CAAGGCCGGC
1021 TGGAACAAGA CCCTGCAGCA GGTGGCCAAG AAGCTGGGCG ACCTGTTCAA CCAGACCACC
1081 ATCATCTTCA AGCCCAGCAG CGGCGGCGAC CCCGAGATCA CCACCCACAG CTTCAACTGC
1141 GGCGGCGAGT TCTTCTACTG CAACACCAGC AAGCTGTTCA ACAGCGCCTG GAACGACAGC
1201 ACCTGGAACA TCGGCAACAA CAACACCGGC AGCGACAACG AGACCATCAT CATCCCCTGC
1261 CGCATCAAGC AGATCATCAA CATGTGGCAG GGCGTGGGCA AGGCCATGTA CGCCCCCCCC
1321 ATCGAGGGCT GGATCAACTG CGCCAGCAAC ATCACCGGCC TGCTGCTGGT GCGCGACGGC
1381 GGCGGCGCCA ACGACAGCCA GAACGAGACC TTCCGCCCCC AGGGCGGCGA CATGCGCGAC
1441 AACTGGCGCA GCGAGCTGTA CAAGTACAAG GTGGTGAAGA TCGAGCCCCT GGGCATCGCC
1501 CCCACCAAGG CCAAGCGCCG CGTGGTGGAG CGCGAGAAGC GCGCCATCGG CCTGGGCGCC
1561 ATGTTCCTGG GCTTCCTGGG CGCCGCCGGC AGCACCATGG GCGCCGCCAG CCTGACCCTG
1621 ACCGTGCAGG CCCGCCAGCT GCTGAGCGGC ATCGTGCAGC ACCAGAACAA CCTGCTGATG
1681 GCCATCGAGG CCCAGCAGCA CCTGCTGCAG CTGACCGTGT GGGGCATCAA GCAGCTGCAG
1741 GCCCGCATCC TGGCCGTGGA GCGCTACCTG CAGGACCAGC AGCTGCTGGG CAGCTGGGGC
1801 TGCAGCGGCC GCCACATCTG CACCACCACC GTGCCCTGGA ACAGCAGCTG GAGCAACAAG
1861 AGCATCGACG ACATCTGGAA CAACATGACC TGGATGGAGT GGGAGAAGGA GATCGACAAC
1921 TACACCGGCG TGATCTACCG CCTGATCGAG GAGAGCCAGA CCCAGCAGGA GAAGAACGAG
1981 CAGGAGCTGC TGCAGCTGGA CAAGTGGGCC AGCCTGTGGA ACTGGTTCAG CATCACCAAG
2041 TGGCTGTGGT ACATCAAGAT CTTCATCATG ATCGTGGGCG GCCTGATCGG CCTGCGCATC
2101 GTGTTCACCG TGCTGAGCCT GGTGAACCGC GTGCGCCAGG GCTACAGCCC CCTGAGCTTC
2161 CAGACCCTGT TCCCCGCCCC CCGCGGCCCC GACCGCCCCG AGGAGATCGA GGAGGGCGGC
2221 GGCGAGCAGG GCCGCGGCCG CAGCACCCGC CTGGTGAACG GCTTCAGCAC CCTGATCTGG
2281 GACGACCTGC GCAACCTGTG CCTGTTCAGC TACCACCGCC TGCGCGACCT GATCCTGATC
2341 GCCACCCGCA TCGTGGAGCT GCTGGGCCGC CGCGGCTGGG AGGCCATCAA GTACCTGTGG
2401 AACCTGCTGC AGTACTGGAG CCAGGAGCTG AAGACCAGCG CCATCAGCCT GTTCAACGCC
2461 ACCGCCGTGG CCGTGGCCGA GGGCACCGAC CGCGTGATCG AGGTGGTGCA GCGCTTCTTC
2521 CGCGGCATCC TGAACGTGCC CACCCGCATC CGCCAGGGCC TGGAGCGCGC CCTGCTGTAA
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FIGURE 15
gp160mod.94UG114

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   1 ATGCGCGTGC GCGAGACCAA GCGCAACTAC CAGCACCTGT GGAAGTGGGG CACCATGCTG
  61 CTGGGCATGC TGATGATCTG CAGCGTGACC GGCAAGAGCT GGGTGACCGT GTACTACGGC
 121 GTGCCCGTGT GGAAGGAGGC CACCACCACC CTGTTCTGCG CCAGCGACGC CAAGGCCTAC
 181 AAGGCCGAGG CCCACAACAT CTGGGCCACC CACGCCTGCG TGCCCACCGA CCCCAACCCC
 241 CAGGAGATCA AGCTGGAGAA CGTGACCGAG AACTTCAACA TGTGGAAGAA CAACATGGTG
 301 GAGCAGATGC ACGAGGACAT CATCAGCCTG TGGGACCAGA GCCTGAAGCC CTGCGTGAAG
 361 CTGACCCCCC TGTGCGTGAC CCTGAACTGC ACCAACTGGG TGACCGACAC CACCAACACC
 421 ACCGGCATGG CCAACTGCAG CTTCAACATC ACCACCGAGA TCCGCGACAA GAAGAAGCAG
 481 GTGCAGGCCC TGTTCTACAA GCTGGACGTG GTGAAGATCA ACGACAACGA CAGCGACAAC
 541 ACCAGCTACC GCCTGATCAA CTGCAACACC AGCGCCATCA CCCAGGCCTG CCCCAAGATG
 601 ACCTTCGAGC CCATCCCCAT CCACTACTGC GCCCCCGCCG GCTTCGCCAT CCTGAAGTGC
 661 AACGAGAAGA AGTTCAACGG CACCGGCCCC TGCAAGAACG TGAGCACCGT GCAGTGCACC
 721 CACGGCATCA GCCCCGTGGT GAGCACCCAG CTGCTGCTGA ACGGCAGCCT GGCCGAGGAG
 781 GAGATCATCA TCCGCAGCGA GAACCTGACC AACAACGCCA AGATCATCAT CGTGCAGCTG
 841 AACGAGAGCG TGCCCATCAA CTGCATCCGC CCCTACAACA CACCCGCCA GAGCACCCGC
 901 ATCGGCCCCG CCAGGCCCT GTTCACCACC AAGGTGATCG GCGACATCCG CCAGGCCCAC
 961 TGCAACATCA GCGGCGCCGG CTGGAACAAG ACCCTGCAGC AGGTGGCCGA GAAGCTGGGC
1021 AACCTGCTGA ACCAGACCAC CATCATCTTC AAGCCCAGCA GCGGCGGCGA CCCCGAGATC
1081 ACCACCCACA GCTTCAACTG CGGCGGCGAG TTCTTCTACT GCAACACCAC CCGCCTGTTC
1141 AACAGCACCT GGAAGCGCAA CAACACGAGC TGGCGCAGCG ACAACACCCC CGACGAGACC
1201 ATCACCCTGC AGTGCCGCAT CAAGCAGATC ATCAACATGT GGCAGGAGGT GGGCAAGGCC
1261 ATGTACGCCC CCCCCATCGA GGGCTTCATC AACTGCAGCA GCAACATCAC CGGCCTGCTG
1321 CTGACCCGCG ACGGCGGCGC CATCAACAGC AGCCAGAACG AGACCTTCCG CCCCGGCGGC
1381 GGCGACATGC GCAACAACTG CGCCAGCGAG CTGTACAAGT ACAAGGTGGT GAAGCTGGAG
1441 CCCATCGGCC TGGCCCCCAC CGCCGCCAAG CGCCGCGTGG TGGAGCGCGA GAAGCGCGCC
1501 ATCGGCCTGG CGCCCTGTT CCTGGGCTTC CTGGGCGCAG CCGGCAGCAC CATGGGCGCC
1561 GTGAGCCTGA CCCTGACCGT GCAGGCCCGC CAGGTGCTGA GCGGCATCGT GCAGCAGCAG
1621 AACAACCTGC TGCGCGCCAT CGAGGCCCAG CAGCACCTGC TGCAGCTGAC CGTGTGGGGC
1681 ATCAAGCAGC TGCAGGCCCG CATCCTGGCC GTGGAGAGCT ACCTGAAGGA CCAGCAGCTG
1741 CTGGGCATCT GGGGCTGCAG CGGCAAGCAC ATCTGCACCA CCAACGTGCC CTGGAACAGC
1801 AGCTGGAGCA ACCGCAGCGT GGACGAGATC TGGAACAACA TGACCTGGAT GGAGTGGGAG
1861 CGCGAGATCG ACAACTACAC CGAGCTGGTG TACAGCCTGC TGGAGGTGAG CCAGATCCAG
1921 CAGGAGAAGA ACGAGCAGGA GCTGCTGAAG CTGGACACCT GGGCCAGCCT GTGGAACTGG
1981 TTCAGCATCA CCCAGTGGCT GTGGTACATC AAGATCTTCA TCATGATCGT GGGCGGCCTG
2041 ATCGGCCTGC GCATCGTGTT CGCCGTGCTG AGCGTGGTGA ACCGCGTGCG CCAGGGCTAC
2101 AGCCCCCTGA GCTTCCAGAC CCTGCTGCCC GCCCCCCGCG AGCCCGACCG CCCCGAGGGC
2161 ATCGAGGAGG AGGGCGGCGA GCGCGACCGC GGCCGCAGCA TCCGCCTGGT GAACGGCCTG
2221 AGCGCCCTGA TCTGGGACGA CCTGCGCAAC CTGTGCCTGT TCAGCTACCA CCGCCTGCGC
2281 GACCTGATCC TGATCGCCGC CCGCATCGTG GAGCTGCTGG GCCGCCGCGG CTGGGAGGCC
2341 ATCAAGTACC TGTGGAACCT GCTGCAGTAC TGGATCCAGG AGCTGAAGAA CAGCGCCGTG
2401 AGCCTGTTCA ACACCATCGC CATCGCCGTG GCCGAGGGCA CCGACCGCGC CATCGAGCTG
2461 GTGCAGCGCG CCGTGCGCGC CATCCTGAAC ATCCCCGTGC GCATCCGCCA GGGCCTGGAG
2521 CGCGCCCTGC TGTAA
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FIGURE 16

gp160mod.ELI

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   1 ATGCGCGCCC GCGGCATCGA GCGCAACTGC CAGAACTGGT GGAAGTGGGG CATCATGCTG
  61 CTGGGCATCC TGATGACCTG CAGCGCCGCC GACAACCTGT GGGTGACCGT GTACTACGGC
 121 GTGCCCGTGT GGAAGGAGGC CACCACCACC CTGTTCTGCG CCAGCGACGC CAAGAGCTAC
 181 GAGACCGAGG CCCACAACAT CTGGGCCACC CACGCCTGCG TGCCCACCGA CCCCAACCCC
 241 CAGGAGATCG CCCTGGAGAA CGTGACCGAG AACTTCAACA TGTGGAAGAA CAACATGGTG
 301 GAGCAGATGC ACGAGGACAT CATCAGCCTG TGGGACCAGA GCCTGAAGCC CTGCGTGAAG
 361 CTGACCCCCC TGTGCGTGAC CCTGAACTGC AGCGACGAGC TGCGCAACAA CGGCACCATG
 421 GGCAACAACG TGACCACCGA GGAGAAGGGC ATGAAGAACT GCAGCTTCAA CGTGACCACC
 481 GTGCTGAAGG ACAAGAAGCA GCAGGTGTAC GCCCTGTTCT ACCGCCTGGA CATCGTGCCC
 541 ATCGACAACG ACAGCAGCAC CAACAGCACC AACTACCGCC TGATCAACTG CAACACCAGC
 601 GCCATCACCC AGGCCTGCCC CAAGGTGAGC TTCGAGCCCA TCCCCATCCA CTACTGCGCC
 661 CCCGCCGGCT TCGCCATCCT GAAGTGCCGC GACAAGAAGT TCAACGGCAC CGGCCCCTGC
 721 ACCAACGTGA GCACCGTGCA GTGCACCCAC GGCATCCGCC CCGTGGTGAG CACCCAGCTG
 781 CTGCTGAACG GCAGCCTGGC CGAGGAGGAG GTGATCATCC GCAGCGAGAA CCTGACCAAC
 841 AACGCCAAGA ACATCATCGC CCACCTGAAC GAGAGCGTGA AGATCACCTG CGCCCGCCCC
 901 TACCAGAACA CCCGCCAGCG CACCCCCATC GGCCTGGGCC AGAGCCTGTA CACCACCCGC
 961 AGCCGCAGCA TCATCGGCCA GGCCCACTGC AACATCAGCC GCGCCCAGTG GAGCAAGACC
1021 CTGCAGCAGG TGGCCCGCAA GCTGGGCACC CTGCTGAACA AGACCATCAT CAAGTTCAAG
1081 CCCAGCAGCG GCGGCGACCC CGAGATCACC ACCCACAGCT TCAACTGCGG CGGCGAGTTC
1141 TTCTACTGCA ACACCAGCGG CCTGTTCAAC AGCACCTGGA ACATCAGCGC CTGGAACAAC
1201 ATCACCGAGA GCAACAACAG CACCAACACC AACATCACCC TGCAGTGCCG CATCAAGCAG
1261 ATCATCAAGA TGGTGGCCGG CCGCAAGGCC ATCTACGCCC CCCCCATCGA GCGCAACATC
1321 CTGTGCAGCA GCAACATCAC CGGCCTGCTG CTGACCCGCG ACGGCGGCAT CAACAACAGC
1381 ACCAACGAGA CCTTCCGCCC CGGCGGCGGC GACATGCGCG ACAACTGGCG CAGCGAGCTG
1441 TACAAGTACA AGGTGGTGCA GATCGAGCCC CTGGGCGTGG CCCCCACCCG CGCCAAGCGC
1501 CGCGTGGTGG AGCGCGAGAA GCGCGCCATC GGCCTGGGCG CCATGTTCCT GGGCTTCCTG
1561 GGCGCCGCCG GCAGCACCAT GGGCGCCCGC AGCGTGACCC TGACCGTGCA GGCCCGCCAG
1621 CTGATGAGCG GCATCGTGCA GCAGCAGAAC AACCTGCTGC GCGCCATCGA GGCCCAGCAG
1681 CACCTGCTGC AGCTGACCGT GTGGGGCATC AAGCAGCTGC AGGCCCGCAT CCTGGCCGTG
1741 GAGCGCTACC TGAAGGACCA GCAGCTGCTG GGCATCTGGG GCTGCAGCGG CAAGCACATC
1801 TGCACCACCA CGTGCCCTG GAACAGCAGC TGGAGCAACC GCAGCCTGAA CGAGATCTGG
1861 CAGAACATGA CCTGGATGGA GTGGGAGCGC GAGATCGACA ACTACACCGG CCTGATCTAC
1921 AGCCTGATCG AGGAGAGCCA GACCCAGCAG GAGAAGAACG AGAAGGAGCT GCTGGAGCTG
1981 GACAAGTGGG CCAGCCTGTG GAACTGGTTC AGCATCACCC AGTGGCTGTG GTACATCAAG
2041 ATCTTCATCA TGATCATCGG CGGCCTGATC GGCCTGCGCA TCGTGTTCGC CGTGCTGAGC
2101 CTGGTGAACC GCGTGCGCCA GGGCTACAGC CCCCTGAGCT TCCAGACCCT GCTGCCCGCC
2161 CCCCGCGGCC CCGACCGCCC CGAGGGCACC GAGGAGGAGG CGGCGAGCG CGGCCGCGAC
2221 CGCAGCGTGC GCCTGCTGAA CGGCTTCAGC GCCCTGATCT GGGACGACCT GCGCAGCCTG
2281 TGCCTGTTCA GCTACCACCG CCTGCGCGAC CTGATCCTGA TCGCCGTGCG CATCGTGGAG
2341 CTGCTGGGCC GCCGCGGCTG GGACATCCTG AAGTACCTGT GGAACCTGCT GCAGTACTGG
2401 AGCCAGGAGC TGCGCAACAG CGCCAGCAGC CTGTTCGACG CCATCGCCAT CGCCGTGGCC
2461 GAGGGCACCG ACCGCGTGAT CGAGATCATC CAGCGCGCCT GCCGCGCCGT GCTGAACATC
2521 CCCCGCCGCA TCCGCCAGGG CCTGGAGCGC AGCCTGCTGT AA
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FIGURE 17

gp160mod.93IN101

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   1 ATGCGCGTGC GCGGCACCCT GCGCAACTAC CAGCAGTGGT GGATCTGGGG CGTGCTGGGC
  61 TTCTGGATGC TGATGATCTG CAACGGCGGC GGCAACCTGT GGGTGACCGT GTACTACGGC
 121 GTGCCCGTGT GGAAGGAGGC CAAGACCACC CTGCTGTGCG CCAGCGACGC CAAGGCCTAC
 181 GAGCGCGAGG TGCACAACGT GTGGGCCACC CACGCCTGCG TGCCCACCGA CCCCAACCCC
 241 CAGGAGATCG TGCTGGGCAA CGTGACCGAG AACTTCAACA TGTGGAAGAA CGACATGGTG
 301 GACCAGATGC ACGAGGACGT GATCAGCCTG TGGGACCAGA GCCTGAAGCC CTGCGTGAAG
 361 CTGACCCCCC TGTGCGTGAC CCTGGAGTGC CGCAACGTGA CCGCAACGT GAGCAGCTAC
 421 AACACCTACA ACGGCAGCGT GGAGGAGATC AAGAACTGCA GCTTCAACGC CACCCCCGAG
 481 GTGCGCGACC GCAAGCAGCG CATGTACGCC CTGTTCTACG GCCTGGACAT CGTGCCCCTG
 541 AACAAGAAGA ACAGCAGCGA GAACAGCAGC GAGTACCGCC TGATCAACTG CAACACCAGC
 601 GCCATCACCC AGGCCTGCCC CAAGGTGACC TTCGACCCCA TCCCCATCCA CTACTGCGCC
 661 CCCGCCGGCT ACGCCATCCT GAAGTGCAAC AACAAGACCT TCAACGGCAC CGGCCCCTGC
 721 AACAACGTGA GCACCGTGCA GTGCACCCAC GGCATCAAGC CCGTGGTGAG CACCCAGCTG
 781 CTGCTGAACG GCAGCCTGGC CGAGGGCGAG ATCATCATCC GCAGCGAGAA CCTGACCAAC
 841 AACGTGAAGA CCATCATCGT GCACCTGAAC CAGAGCGTGG AGATCGTGTG CACCCGCCCC
 901 AACAACAACA CCCGCAAGAG CATCCGCATC GGCCCCGGCC AGACCTTCTA CGCCACCGGC
 961 GACATCATCG GCGACATCCG CCAGGCCCAC TGCAACATCA GCCGCGACAA GTGGAACGAG
1021 ACCCTGCAGC GCGTGGGCAA GAAGCTGGCC GAGCACTTCC ACAACAAGAC CATCAAGTTC
1081 GCCAGCAGCA GCGGCGGCGA CCTGGAGATC ACCACCCACA GCTTCAACTG CCGCGGCGAG
1141 TTCTTCTACT GCAACACCAG CGGCCTGTTC AACGGCACCT ACATGCCCAC CTACATGCCC
1201 AACGGCACCG AGAGCAACAG CAACAGCACC ATCACCATCC CCTGCCGCAT CAAGCAGATC
1261 ATCAACATGT GGCAGGAGGT GGGCCGCGCC ATGTACGCCC CCCCCATCGC CGGCAACATC
1321 ACCTGCACCA GCAACATCAC CGGCCTGCTG CTGGTGCACG ACGGCGGCAT CAAGGAGAAC
1381 GACACCGAGA ACAAGACCGA GATCTTCCGC CCCGGCGGCG GCGACATGCG CGACAACTGG
1441 CGCAGCGAGC TGTACAAGTA CAAGGTGGTG GAGATCAAGC CCCTGGGCGT GGCCCCCACC
1501 GCCGCCAAGC GCCGCGTGGT GGAGCGCGAG AAGCGCGCCG TGGGCATCGG CGCCGTGTTC
1561 CTGGGCTTCC TGGGCGCCGC CGGCAGCACC ATGGGCGCCG CCAGCATCAC CCTGACCGCC
1621 CAGGCCCGCC AGCTGCTGAG CGGCATCGTG CAGCAGCAGA GCAACCTGCT GCGCGCCATC
1681 GAGGCCCAGC AGCACCTGCT GCAGCTGACC GTGTGGGGCA TCAAGCAGCT GCAGACCCGC
1741 GTGCTGGCCA TCGAGCGCTA CCTGAAGGAC CAGCAGCTGC TGGGCATCTG GGGCTGCAGC
1801 GGCAAGCTGA TCTGCACCAC CGCCGTGCCC TGGAACGCA GCTGGAGCAA CAAGACCCAG
1861 AGCGAGATCT GGAACAACAT GACCTGGATG CAGTGGGACC GCGAGGTGAG CAACTACACC
1921 AACATCATCT ACAGCCTGCT GGAGGAGAGC CAGAACCAGC AGGAGAAGAA CGAGAAGGAC
1981 CTGCTGGCCC TGGACAGCTG GAAGAACCTG TGGAGCTGGT CGACATCAC CAACTGGCTG
2041 TGGTACATCA AGATCTTCAT CATGATCGTG GGCGGCCTGA TCGGCCTGCG CATCATCTTC
2101 GCCGTGCTGA GCATCGTGAA CCGCGTGCGC CAGGGCTACA GCCCCCTGAG CTTCCAGACC
2161 CTGACCCCCA ACCCCCGCGG CCCCGACCGC CTGGGCCGCA TCGAGGAGGA GGGCGGCGAG
2221 CAGGACAAGG ACCGCAGCAT CCGCCTGGTG AACGGCTTCC TGGCCCTGGC CTGGGACGAC
2281 CTGCGCAACC TGTGCCTGTT CAGCTACCAC CGCCTGCGCG ACTTCATCAG CGTGGCCGCC
2341 CGCGTGGTGG AGCTGCTGGG CCGCAGCAGC TGGGAGGCCC TGAAGTACCT GGGCAGCCTG
2401 GTGCAGTACT GGGGCCTGGA GCTGAAGAAG AGCGCCATCA GCCTGTTCGA CAGCATCGCC
2461 ATCGTGGTGG CCGAGGGCAC CGACCGCATC ATCGAGCTGG TGCAGGGCTT CTGCCGCGCC
2521 ATCCGCAACA TCCCCACCCG CATCCGCCAG GGCTTCGAGG CCGCCCTGCA GTAA
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FIGURE 18

gp160mod.cm235.V3con

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   1 ATGGATGCAA TGAAGAGAGG GCTCTGCTGT GTGCTGCTGC TGTGTGGAGC AGTCTTCGTT
  61 TCGCCCAGCG CTAGCAACAA CCTGTGGGTG ACCGTGTACT ACGGCGTGCC CGTGTGGCGC
 121 GACGCCGACA CCACCCTGTT CTGCGCCAGC GACGCCAAGG CCCACGAGAC CGAGGTGCAC
 181 AACGTGTGGG CCACCCACGC CTGCGTGCCC ACCGACCCCA ACCCCCAGGA GATCCACCTG
 241 GAGAACGTGA CCGAGAACTT CAACATGTGG AAGAACAACA TGGTGGAGCA GATGCAGGAG
 301 GACGTGATCA GCCTGTGGGA CCAGAGCCTG AAGCCCTGCG TGAAGCTGAC CCCCCTGTGC
 361 GTGACCCTGA ACTGCACCAA CGCCAAGCTG ACCAACGTGA ACAACATCAC CAGCGTGAGC
 421 AACACCATCG GCAACATCAC CGACGAGGTG CGCAACTGCA GCTTCAACAT GACCACCGAG
 481 CTGCGCGACA AGAAGCAGAA GGTGCACGCC CTGTTCTACA AGCTGGACAT CGTGCCCATC
 541 GAGGACAACA AGACCAGCAG CGAGTACCGC CTGATCAACT GCAACACCAG CGTGATCAAG
 601 CAGGCCTGCC CCAAGATCAG CTTCGACCCC ATCCCCATCC ACTACTGCAC CCCCGCCGGC
 661 TACGCCATCC TGAAGTGCAA CGACAAGAAC TTCAACGGCA CCGGCCCCTG CAAGAACGTG
 721 AGCAGCGTGC AGTGCACCCA CGGCATCAAG CCCGTGGTGA GCACCCAGCT GCTGCTGAAC
 781 GGCAGCCTGG CCGAGGAGGA GATCATCATC CGCAGCGAGA ACCTGACCAA CAACGCCAAG
 841 ACCATCATCG TGCACCTGAA CAAGAGCGTG GAGATCAACT GCACCCGCCC CAGCAACAAC
 901 ACCCGCACCA GCATCACCAT CGGCCCCGGC CAGGTGTTCT ACCGCACCGG CGACATCATC
 961 GGCGACATCC GCAAGGCCTA CTGCGAGATC AACGGCACCA GTGGAACGA GGTGCTGACC
1021 CAGGTGACCG AGAAGCTGAA GGAGCACTTC AACAACAAGA CCATCATCTT CCAGCCCCCC
1081 AGCGGCGGCG ACCTGGAGAT CACCATGCAC CACTTCAACT GCCGCGGCGA GTTCTTCTAC
1141 TGCAACACCA CCCGCCTGTT CAACAACACC TGCATCGAGA ACGGCACCAT GGGCGGCTGC
1201 AACGGCACCA TCATCCTGCC CTGCAAGATC AAGCAGATCA TCAACATGTG GCAGGGCGCC
1261 GGCCAGGCCA TGTACGCCCC CCCCATCAGC GGCCGCATCA ACTGCGTGAG CAACATCACC
1321 GGCATCCTGC TGACCCGCGA CGGCGGCGCC ATCAACACCA CCAACGAGAC CTTCCGCCCC
1381 GGCGGCGGCA ACATCAAGGA CAACTGGCGC AGCGAGCTGT ACAAGTACAA GGTGGTGCAG
1441 ATCGAGCCCC TGGGCATCGC CCCCACCCGC GCCAAGCGCC GCGTGGTGGA GCGCGAGAAG
1501 CGCGCCGTGG GCATCGGCGC CATGATCTTC GGCTTCCTGG GCGCCGCCGG CAGCACCATG
1561 GGCGCCGCCA GCATCACCCT GACCGTGCAG GCCCGCCAGC TGCTGAGCGG CATCGTGCAG
1621 CAGCAGAGCA ACCTGCTGCG CGCCATCGAG GCCCAGCAGC ACCTGCTGCA GCTGACCGTG
1681 TGGGGCATCA AGCAGCTGCA GGCCCGCGTG CTGGCCGTGA GCGCTACCT GAAGGACCAG
1741 AAGTTCCTGG GCCTGTGGGG CTGCAGCGGC AAGATCATCT GCACCACCGC CGTGCCCTGG
1801 AACAGCACCT GGAGCAACCG CAGCTACGAG GAGATCTGGA ACAACATGAC CTGGATCGAG
1861 TGGGAGCGCG AGATCAGCAA CTACACCAAC CAGATCTACG AGATCCTGAC CGAGAGCCAG
1921 AACCAGCAGG ACCGCAACGA GAAGGACCTG CTGGAGCTGG ACAAGTGGGC CAGCCTGTGG
1981 AACTGGTTCG ACATCACCAA GTGGCTGTGG TACATCAAGA TCTTCATCAT GATCATCGGC
2041 GGCCTGATCG GCCTGCGCAT CATCTTCGCC GTGCTGAGCA TCGTGAACCG CGTGCGCCAG
2101 GGCTACAGCC CCCTGAGCTT CCAGACCCCC TTCACCACC AGCGCGAGCC CGACCGCAGC
2161 GAGCGCATCG AGGAGGGCGG CGGCGAGCAG GGCCGCGACC GCAGCGTGCG CCTGGTGAGC
2221 GGCTTCCTGG CCCTGGCCTG GGACGACCTG CGCAGCCTGT GCCTGTTCAG CTACCACCGC
2281 CTGCGCGACT TCATCCTGAT CGCCGCCCGC ACCGTGAAGC TGCTGGGCCG CAGCAGCCTG
2341 AAGGGCCTGC GCCGCGGCTG GGAGGGCCTG AAGTACCTGG GCAACCTGCT GCTGTACTGG
2401 GGCCAGGAGC TGAAGATCAG CGCCATCAGC CTGCTGGACG CCACCGCCAT CATCGTGGCC
2461 GGCTGGACCG ACCGCGTGAT CGAGGTGGCC CAGGGCGCCT GGCGCGCCAT CCTGCACATC
2521 CCCCGCCGCA TCCGCCAGGG CCTGGAGCGC ACCCTGCTGT AA
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FIGURE 19
gp160partialmod.cm235.V3 con

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   1 ATGGATGCAA TGAAGAGAGG GCTCTGCTGT GTGCTGCTGC TGTGTGGAGC AGTCTTCGTT
  61 TCGCCCAGCG CTAGCAACAA CTTGTGGGTT ACAGTTTATT ATGGGGTTCC TGTGTGGAGA
 121 GATGCAGATA CCACCCTATT TTGTGCATCA GATGCCAAAG CACATGAGAC AGAAGTGCAC
 181 AATGTCTGGG CCACACATGC CTGTGTACCC ACAGACCCCA ACCCACAAGA AATACACCTG
 241 GAAAATGTAA CAGAAAATTT TAACATGTGG AAAAATAACA TGGTAGAGCA GATGCAGGAG
 301 GATGTAATCA GTTTATGGGA TCAAAGTCTA AAGCCATGTG TAAAGTTAAC TCCTCTCTGC
 361 GTTACTTTAA ATTGTACCAA TGCTAAGTTG ACCAATGTCA ATAACATAAC CAGTGTCTCT
 421 AACACAATAG GAAATATAAC AGATGAAGTA AGAAACTGTT CTTTTAATAT GACCACAGAA
 481 CTAAGAGATA AGAAGCAGAA GGTCCATGCA CTTTTTTATA AGCTTGATAT AGTACCAATT
 541 GAAGATAATA AGACTAGTAG TGAGTATAGG TTAATAAATT GTAATACTTC AGTCATTAAG
 601 CAGGCTTGTC CAAAGATATC CTTTGATCCA ATTCCTATAC ATTATTGTAC TCCAGCTGGT
 661 TATGCGATTT TAAAGTGTAA TGATAAGAAT TTCAATGGGA CAGGGCCATG TAAAAATGTC
 721 AGCTCAGTAC AATGCACACA TGGAATTAAG CCAGTGGTAT CAACTCAATT GCTGTTAAAT
 781 GGCAGTCTAG CAGAAGAAGA GATAATAATC AGATCTGAAA ATCTCACAAA CAATGCCAAA
 841 ACCATAATAG TGCACCTTAA TAAATCTGTA GAAATCAATT GTACCAGACC CTCCAACAAT
 901 ACAAGAACAA GTATAACTAT AGGACCAGGA CAAGTATTCT ATAGAACAGG AGACATAATA
 961 GGAGATATAA GAAAAGCATA TTGTGAGATT AATGGAACAA AATGGAATGA AGTTTTAACA
1021 CAGGTAACTG AAAAATTAAA AGAGCACTTT AATAATAAGA CAATAATCTT TCAACCACCC
1081 TCAGGAGGAG ATCTAGAAAT TACAATGCAT CATTTTAATT GTAGAGGGGA ATTTTTCTAT
1141 TGCAATACAA CACGACTGTT TAATAATACT TGCATAGAAA ATGGAACCAT GGGGGGGTGT
1201 AATGGCACTA TCATACTTCC ATGCAAGATA AAGCAAATTA TAAACATGTG GCAGGGAGCA
1261 GGACAAGCAA TGTATGCTCC TCCCATCAGT GGAAGAATTA ATTGTGTATC AAATATTACA
1321 GGAATACTAT TGACAAGAGA TGGTGGTGCT ATTAATACAA CTAATGAGAC CTTCCGCCCC
1381 GGCGGCGGCA ACATCAAGGA CAACTGGCGC AGCGAGCTGT ACAAGTACAA GGTGGTGCAG
1441 ATCGAGCCCC TGGGCATCGC CCCCACCCGC GCCAAGCGCC GCGTGGTGGA GCGCGAGAAG
1501 CGCGCCGTGG GCATCGGCGC CATGATCTTC GGCTTCCTGG GCGCCGCCGG CAGCACCATG
1561 GGCGCCGCCA GCATCACCCT GACCGTGCAG GCCCGCCAGC TGCTGAGCGG CATCGTGCAG
1621 CAGCAGAGCA ACCTGCTGCG CGCCATCGAG GCCCAGCAGC ACCTGCTGCA GCTGACCGTG
1681 TGGGGCATCA AGCAGCTGCA GGCCCGCGTG CTGGCCGTGG AGCGCTACCT GAAGGACCAG
1741 AAGTTCCTGG GCCTGTGGGG CTGCAGCGGC AAGATCATCT GCACCACCGC CGTGCCCTGG
1801 AACAGCACCT GGAGCAACCG CAGCTACGAG GAGATCTGGA ACAACATGAC CTGGATCGAG
1861 TGGGAGCGCG AGATCAGCAA CTACACCAAC CAGATCTACG AGATCCTGAC CGAGAGCCAG
1921 AACCAGCAGG ACCGCAACGA GAAGGACCTG CTGGAGCTGG ACAAGTGGGC CAGCCTGTGG
1981 AACTGGTTCG ACATCACCAA GTGGCTGTGG TACATCAAAA TATTTATAAT GATAATAGGA
2041 GGGTTAATAG GTTTAAGGAT AATTTTTGCT GTGCTTTCTA TAGTGAATAG AGTTAGGCAG
2101 GGATACTCAC CTTTGTCTTT CCAGACCCCT TTCCATCATC AGAGGGAACC CGACAGATCC
2161 GAAAGAATCG AAGAAGGAGG TGGCGAGCAA GGCAGAGACA GATCCGTGCG ATTAGTGAGC
2221 GGATTCTTAG CTCTTGCGTG GGACGATCTA CGGAGCCTGT GCCTCTTCAG CTACCACCGC
2281 TTGAGAGACT TCATCTTGAT TGCAGCGAGG ACTGTGAAAC TTCTGGGACG CAGCAGTCTC
2341 AAGGGACTGA GACGGGGGTG GGAAGGTCTC AAATATCTGG GGAATCTTCT GTTATATTGG
2401 GGTCAGGAAC TAAAAATTAG CGCTATTTCT TTGCTTGATG CTACAGCAAT AATAGTAGCG
2461 GGGTGGACAG ATAGGGTTAT AGAAGTAGCA CAAGGAGCTT GGAGAGCCAT TCTCCACATA
2521 CCTAGGAGAA TCAGACAGGG CTTAGAAAGG ACTTTGCTAT AA
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FIGURE 20

Serum Binding Antibody Titers to HIV-1$_{SF162}$ ENV Protein

Immunization	Replication-Competent Ad		Replication-Defective Ad	
	10^7	10^8	10^8	10^8
Post 1st Ad	20	114.11	276.00	46.11
	20	390.91	N/A	72.06
	20	33.31		29.51
Post 2nd Ad	2315.60	4242.53	114	55.57
	14380.44	8251.33	N/A	128.00
	372.87	2181.35		24.13
Post 1st gp140	41175.45	43589.41	906	2675.15
	42411.99	51950.41	N/A	9448.33
	39974.95	36574.05		757.43
Post 2nd gp140	19789.57	65799.55	14176	105578.03
	32906.06	68333.17	N/A	208905.20
	11901.37	63359.86		53357.79

FIGURE 21

Proliferative responses following Ad-HIVenv recombinant priming and HIV$_{SF162}$ oligomeric gp140△V2 boosting
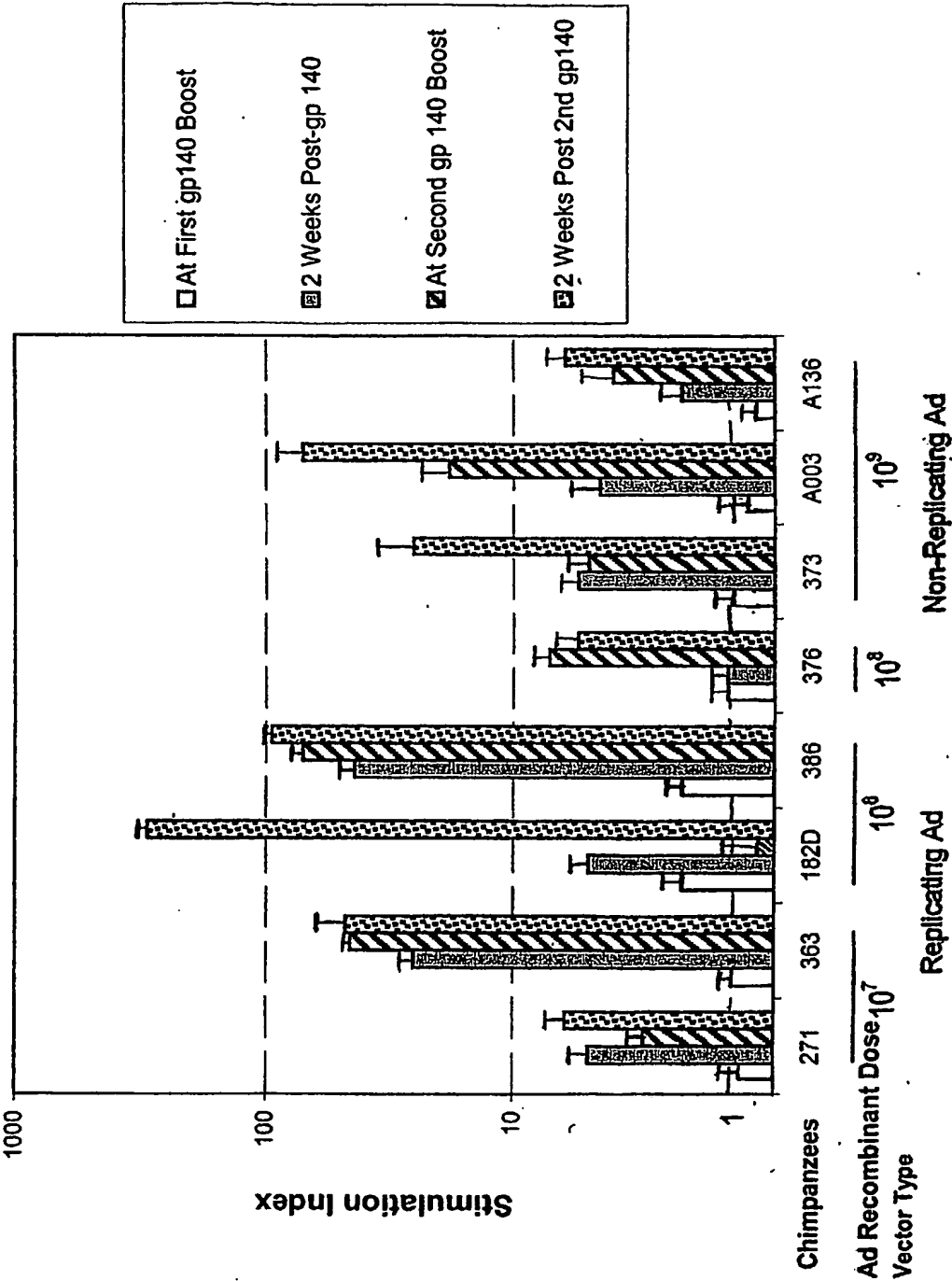
FIGURE 22

Immunization Regimen and Schedule

IN Ad5/HIV-1$_{MN}$ENV	IN Ad7/HIV-1$_{MN}$ENV	IM HIV-1$_{SF162}$gp140ΔV2	IM HIV-1$_{SF162}$gp140ΔV2
0	13	37 (60 ug)	49 (100 ug)

61 weeks
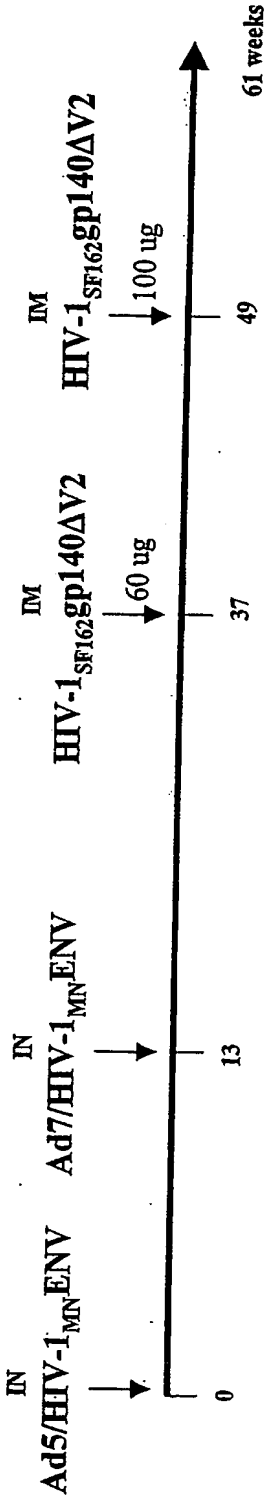
IN = intranasal; IM = intramuscular

Replication-competent Ad Vaccine Group

Chimpanzees	Priming Immunization (dose)
271, 363, A163	Ad5- or Ad7- ΔE3/HIV$_{MN}$Env (10^7 pfu)
182D, 386	Ad5- or Ad7- ΔE3/HIV$_{MN}$Env (10^8 pfu)

Replication-defective Ad Vaccine Group

Chimpanzees	Priming Immunization (dose)
376, 360	Ad5- or Ad7- ΔE1E3/HIV$_{MN}$Env (10^8 pfu)
373, A136, A003	Ad5- or Ad7- ΔE1E3/HIV$_{MN}$Env (10^9 pfu)

Priming with replicating Ad-recombinant results in higher binding antibody titers

FIGURE 23A

Serum Binding Antibody Titers to HIV-1$_{SF162}$ Env Protein

Animal Groups	Dose	2nd Ad wk 15	1st gp140 wk 39	2nd gp140 wk 51
Replicating Ad	10^7	475	3237	13462
Replicating Ad	10^8	4242	43589	65799
Non-replicating Ad	10^8	48	2784	21953
Non-replicating Ad	10^9	56	2672	49005

** Higher titers to gp120 homologous to gp140 boost independent of
** vector (P = 0.0040)

Serum Binding Antibody Titers to HIV-1$_{IIIB}$ Env Protein

Animal Groups	Dose	2nd Ad wk 15	1st gp140 wk 39	2nd gp140 wk 51
Replicating Ad	10^7	397	3794	28360
Replicating Ad	10^8	68	4021	213307
Non-replicating Ad	10^8	10	51	10471
Non-replicating Ad	10^9	22	161	49570

* Higher titers to gp120 heterologous
* to gp140 boost in groups primed with
  replicating Ad-recombinants
  (P = 0.018).

FIGURE 23B

Kinetics of Serum Binding Antibody Titers to HIV-1$_{IIIB}$ Env Protein

Replicating > non-replicating
P = 0.018

Ad-recombinant

gp140@V2
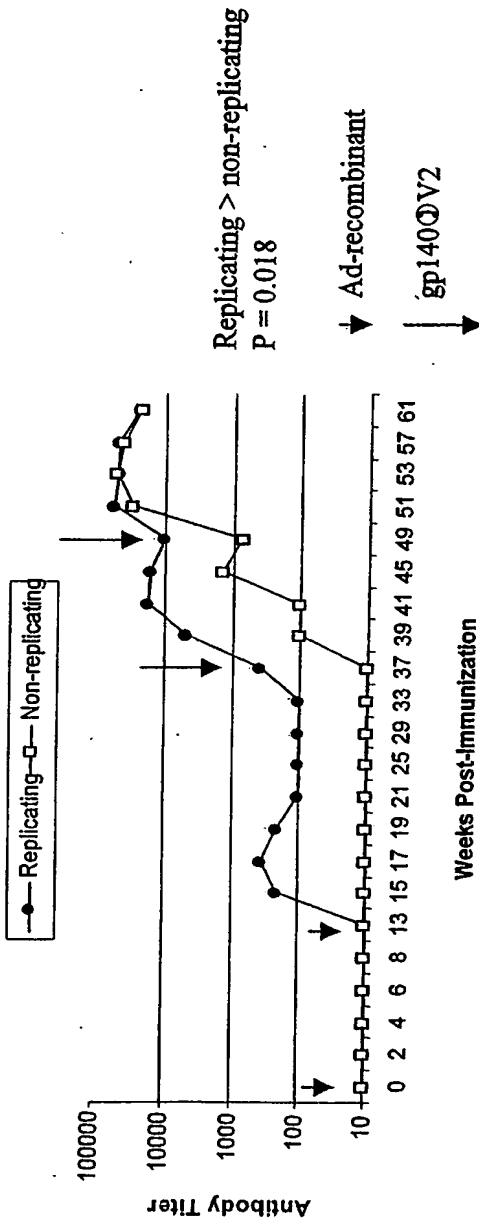
Induction of Cross-Clade Binding Antibodies
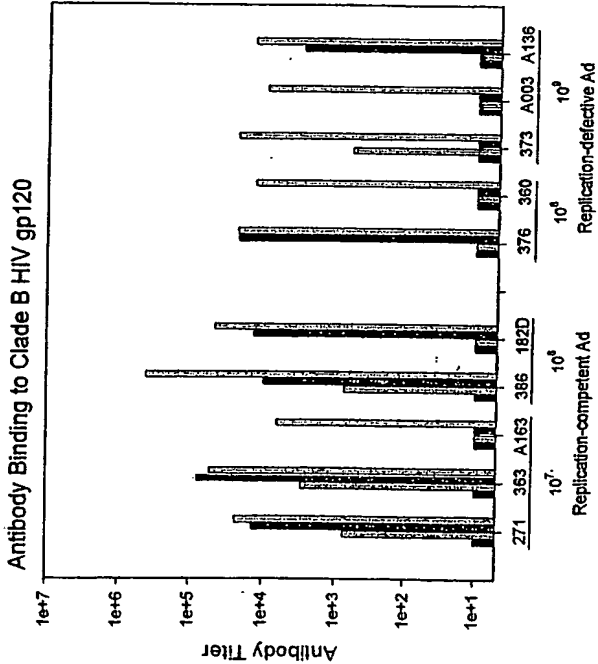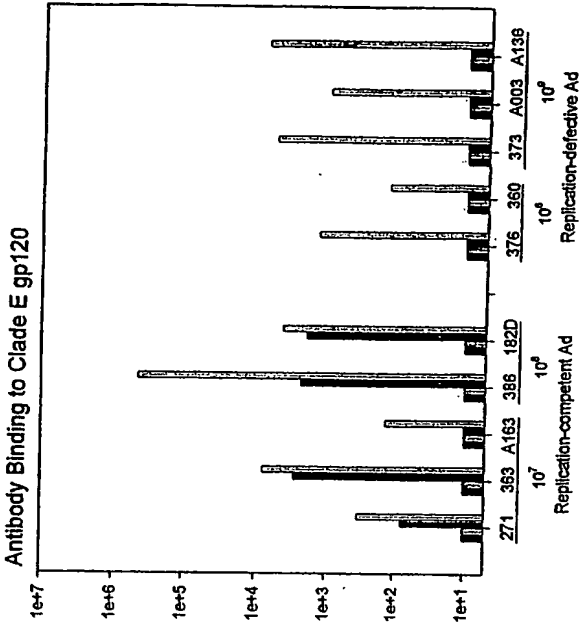

FIGURE 24A
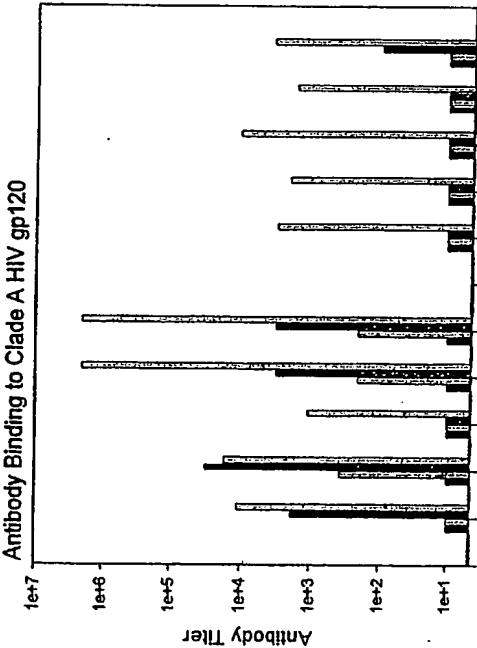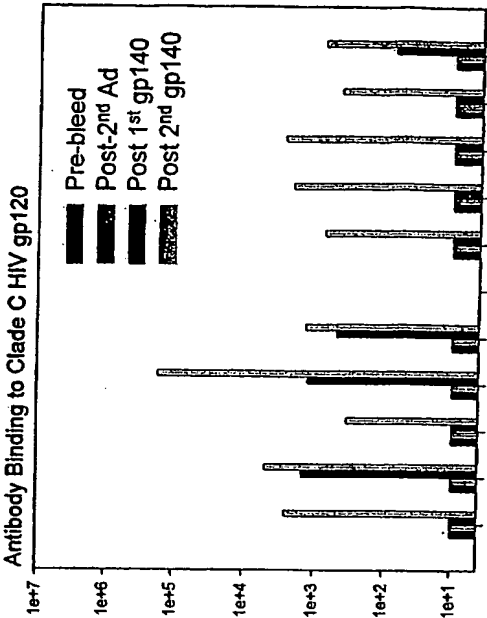
FIGURE 24B

FIGURE 24C

FIGURE 24D

Replicating Ad-HIV recombinants are more effective at priming neutralizing antibody responses
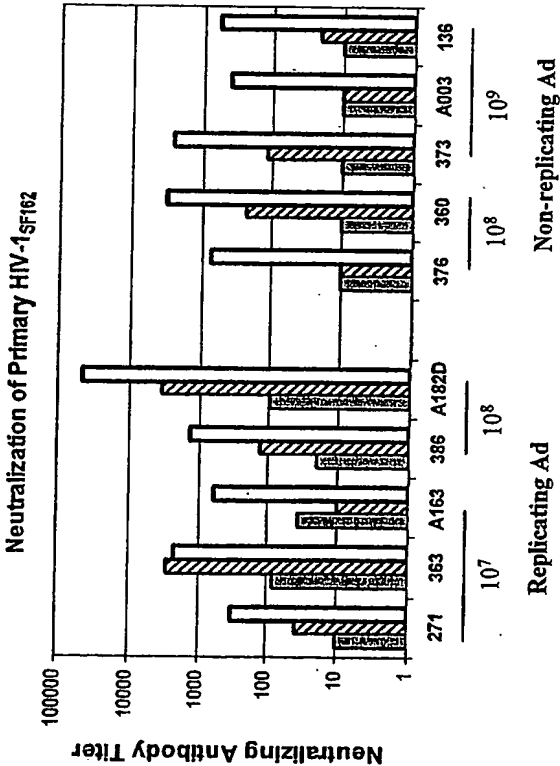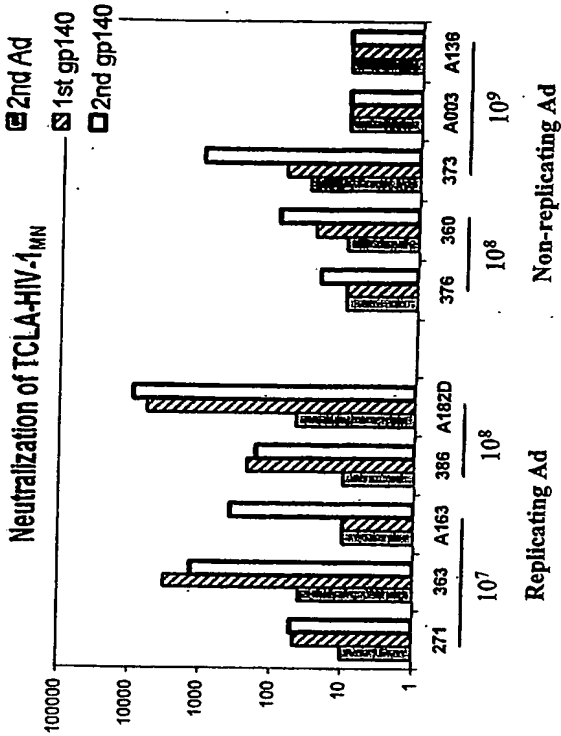
FIGURE 25A

FIGURE 25B

FIGURE 26

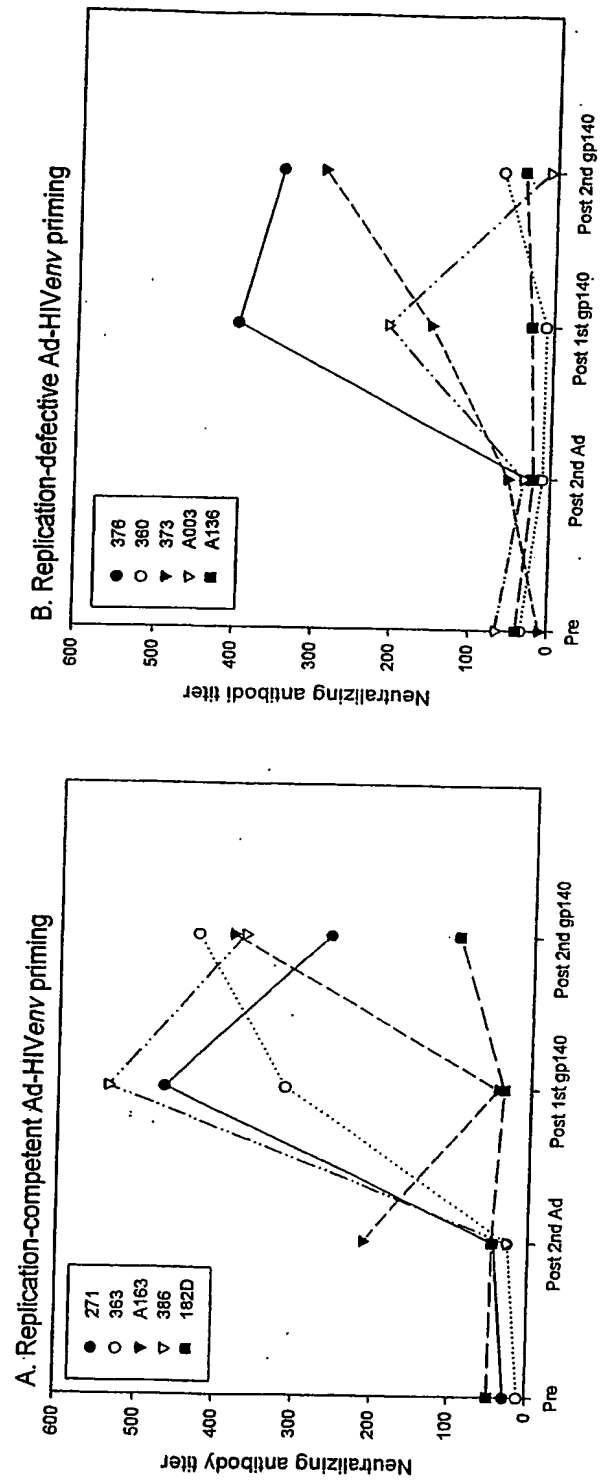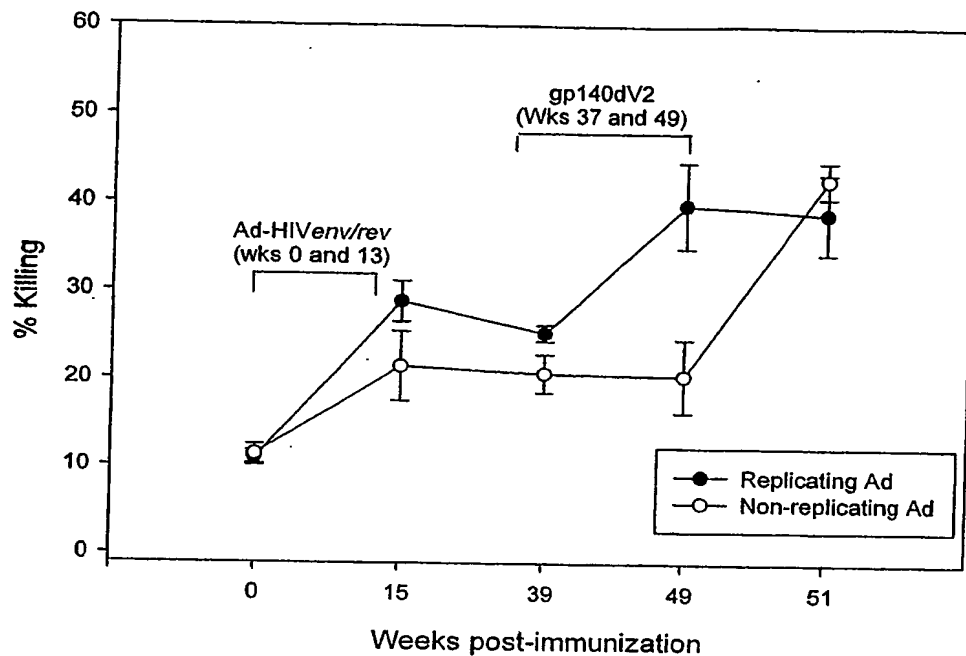Induction of neutralizing antibodies to clade C HIV_{TV-1} following a clade B immunization regimen.

FIGURE 27

Induction of antibody-dependent cellular cytotoxicity (ADCC) activity by an Ad-HIV$_{MN}$env/rev priming/oligomeric gp140dV2 boosting regimen


Weeks post-immunization

Chimpanzees were immunized intranasally with Ad5-HIV$_{MN}$env/rev (wk 0) and with Ad7-HIV$_{MN}$env/rev (wk 13). They were boosted with oligomeric HIV$_{SF162}$ gp140 dV2 in MF-59 adjuvant at weeks 37 and 49. ADCC activity was determined using human PBMC as effectors and HIV$_{IIIB}$ gp120-coated CEM-NK^r cells at an E:T of 50:1. Ten-fold serum dilutions were evaluated. Positive killing was defined as % killing by the negative control + 3 S.D. (20.4%).

A significant increase in % killing over weeks 15 to 51 was seen in chimpanzees primed with the replication-competent Ad-recombinants compared to the replication-defective Ad-recombinants (P = 0.022).

FIGURE 28

Replicating Ad-HIV recombinants are better at priming T-cell proliferative responses than non-replicating Ad-HIV recombinants
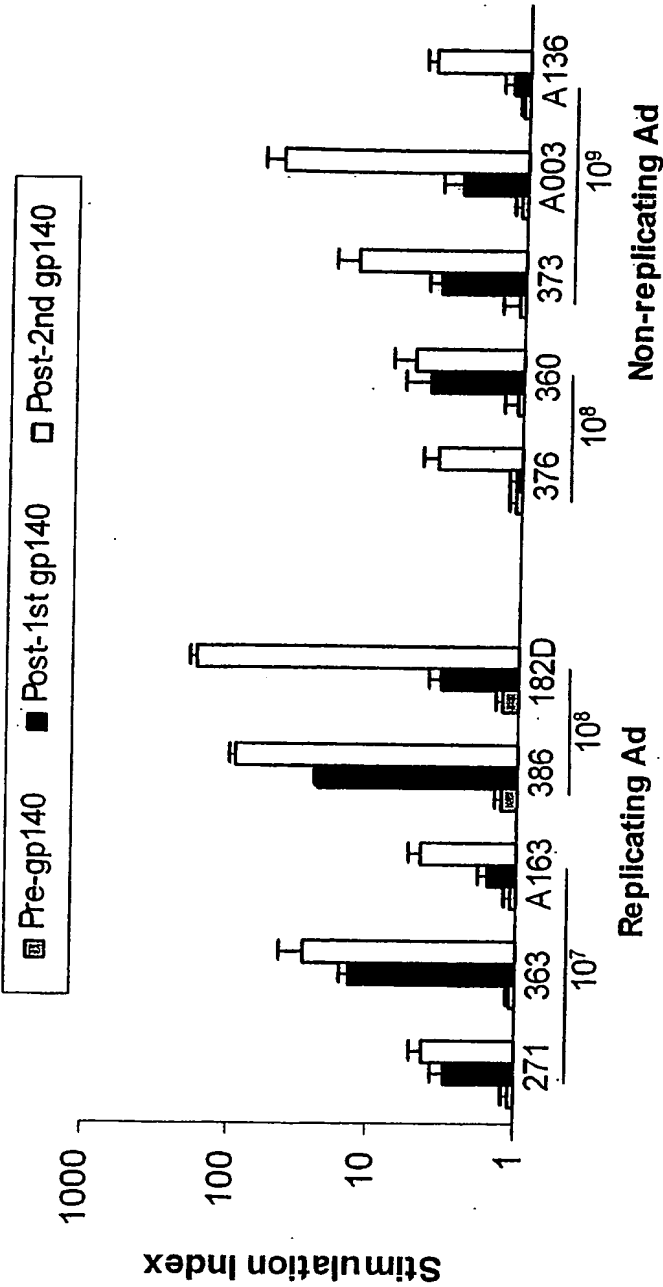
Post-2nd gp140: Replicating > Non-replicating, p = 0.022
Over all 3 time points, there is a linear trend of replicating > non-replicating, p = 0.010

FIGURE 29

Replicating Ad /HIV$_{MN}$*env/rev* Induces More IFN-γ Secreting Cells at the Same or
Lower Dose Compared to Non-replicating Ad /HIV$_{MN}$*env/rev*